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FIG. 41A

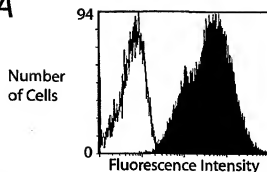


FIG. 41B

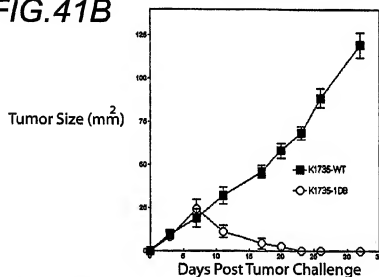
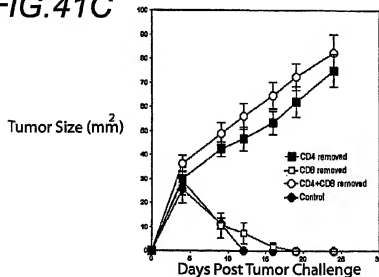
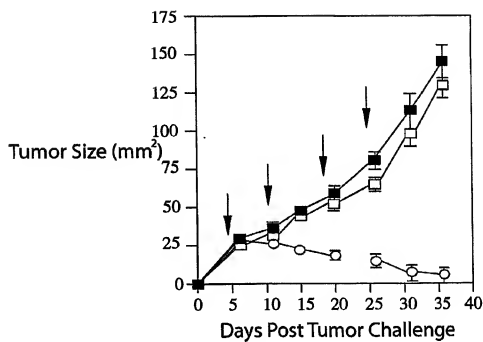


FIG. 41C



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FIG.42



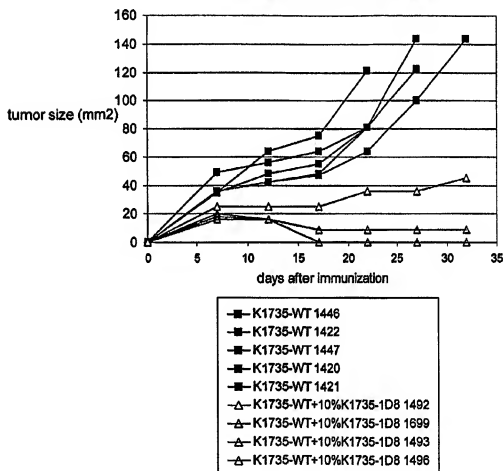
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FIG.43

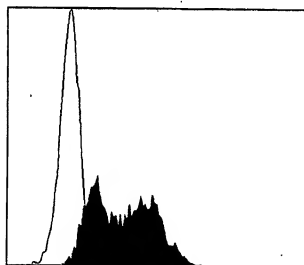
Mixtures of K1735-WT and K1735-1D8 transfected tumor lines
inhibit tumor outgrowth in C3H mice



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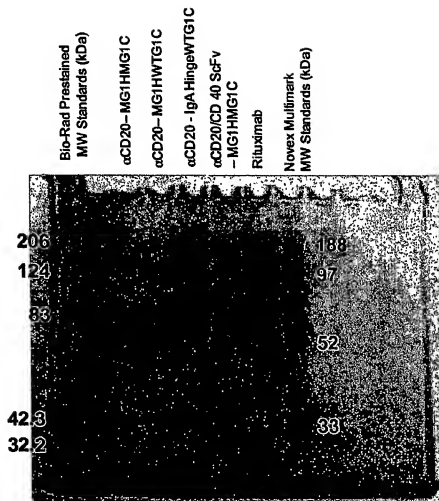
FIG.44

Expression of Anti-CD137 scFvlg on the Surface of
Panned Ag104 Transfected Tumor Cells



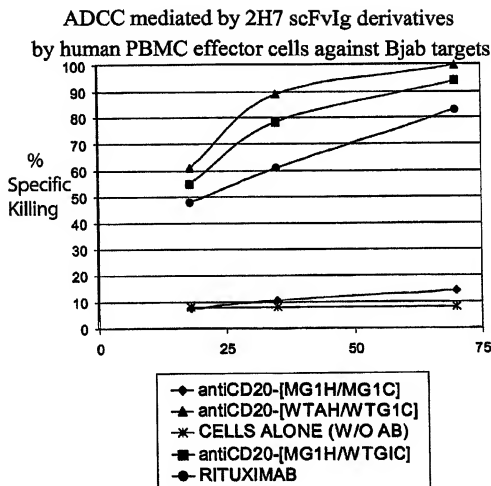
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FIG.45



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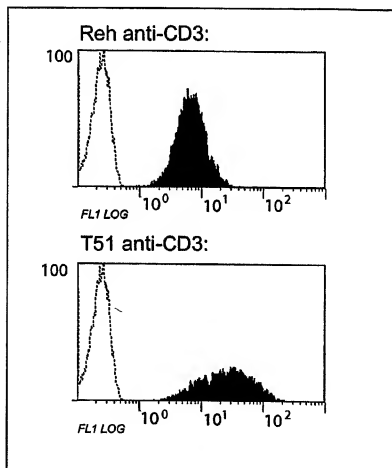
FIG.46



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FIG.47

Cell surface expression of anti-human CD3 scFvIg fusion protein on Reh and T51 Cells.



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FIG. 48A

Targeting of Cytotoxicity to Transfected Cell Lines
by Surface expression of CD3 scFvIg

Cytotoxic activity of resting PBMC towards transfected Reh cells

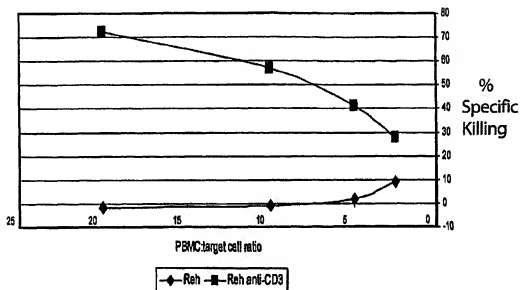
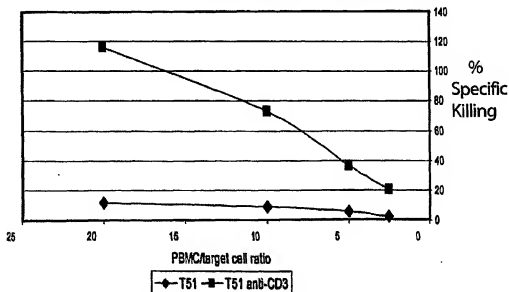


FIG. 48B

Cytotoxic activity of resting PBMC towards transfected T51 lymphoblastoid cells

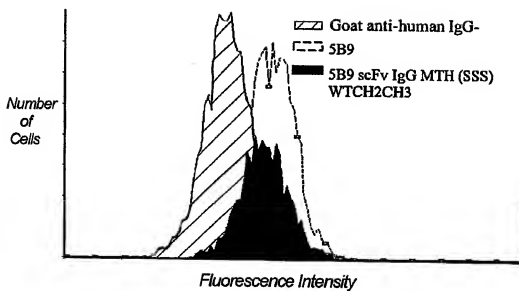


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FIG. 49



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<150> us 10/207,655

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<160> 426

<170> PatentIn version 3.0

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<223> asp-gly3ser(gly4ser)2-ser peptide linker

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<220>
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<223> HINGE CYSTEINES (826-829; 844-847; 853-856) MUTATED TO SERINES
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FUNCTION

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>
<221> v_region
<222> (73)..(405)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<220>
<221> misc_feature
<222> (406)..(450)
<223> SYNTHETIC (GLY4SER)3 LINKER PEPTIDE

<220>
<221> v_region
<222> (454)..(825)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<400> 8
aagcttgccg ccatggagac agacacactc ctgctatggg tgcgtctgct ctgggttcca
60
ggctccactg gtgacattgt gctgacccaa tctccagctt ctttggctgt gtccttaggg
120
cagagggccca ccatctcctg caaggccagc caaagtgttg attatgatgg tgatagttat
180
ttgaactggt accaacagat tccaggacag ccacccaac tcctcatcta tgatgatcc
240
aatctagtgt ctgggatccc acccaggttt agtggcagtg ggtctgggac agacttcacc
300
ctcaacatcc atcctgtgga gaaggtggat gctgcaacct atcactgtca gcaaagtact
360
gaggatccgt ggacgttcgg tggaggcacc aagctggaaa tcaaaggctg cgggtgctcg
420
ggcggtggtg ggtcgggtgg cgcgggatcg tcacagggtc agctgcagca gtcctgggct
480
gagctggtag ggcctgggtc ctcagtgaag atttctcgca aggcttctgg ctatgcattc
540
agtagctact ggatgaactg ggtgaagcag aggcctggac agggctcttga gtggattgga
600
cagatttgcc ctggagatgg tgatactaac tacaatggaa agttcaaggg taaagccact
660
ctgactcgag acgaatcttc cagcacagcc tacatgcaac tcagcagcct agcatctgag
720
gactctgcgg tctatttctg tgcaagacgg gagactacga cggtaggccc ttattactat
780
gctatggact actgggggtca aggaacctca gtcaccgtct ctcca
825

<210> 9
<211> 795
<212> DNA
<213> Artificial Sequence

<220>
<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>
<221> misc_feature
<222> (13)..(72)
<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

<220>
<221> v_region
<222> (73)..(393)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<220>
<221> misc_feature
<222> (394)..(441)
<223> SYNTHETIC LINKER PEPTIDE ENCODED (GLY4SER)3

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<220>
<221> V_region
<222> (442)..(795)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<400> 9
aagcttgccg ccatgggtatc cacagctcag ttccttgggt tgctgctgct gtggcttaca
60
ggtaggcagat gtgacatcca gatgactcag tctccagcct ccttatctgc atctgtggga
120
ggagactgtca ccatcacatg tcgaacaagt gaaatgttt acagttattt ggcttggtat
180
cagcagaaaac agggaaaatc tctcagctc ctggctcttt ttgcaaaaac cttagcagaa
240
gggtgtccat caaggttcag tggcagtga tcaggcacac agttttctct gaagatcagc
300
agcctgcagc ctgaagattc tggaaattat ttctgtcaac atcattccga taatccgtgg
360
acgttcggtg gaggcaccga actggagatc aaaggtggcg gtggctcggg cggtggtggg
420
tcgggtggcg gcggatcgtc agcgggtccag ctgcagcagt ctggacctga gctggaaaag
480
cctggcgctt cagtgaagat ttctgcaag gcttctggtt actcattcac tggctacaat
540
atgaactggg tgaagcagaa taatggaag agccttgagt ggattggaaa tattgatcct
600
tattatgggt gtactaccta caaccggaag ttcaagggca aggccacatt gactgtagac
660
aaattcctcca gcacagccta catgcagctc aagagtctga catctgagga ctctgcagtc
720
tattactgtg caagatcggg cgccctatg gactactggg gtcaaggaac ctcatgacc
780
gtctcttctg atcag
795

<210> 10
<211> 824
<212> DNA
<213> Artificial Sequence

<220>
<223> SYNTHETIC MOUSE FUSION GENE

<220>
<221> sig_peptide
<222> (1)..(61)
<223> native light chain leader peptide

<220>
<221> V_region
<222> (62)..(397)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>
<221> misc_feature
<222> (398)..(445)
<223> (gly4ser)3 linker peptide

<220>
<221> V_region
<222> (445)..(818)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>
<221> misc_feature
<222> (819)..(824)
<223> BclI restriction site

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<400> 10
atggagtcac attcccaggt ctttctctcc ctgctgctct gggatatctgg tacctgtggg
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aacattatga tgacacagtc gccatcatct ctggctgtgt cagcaggaga aaaggtcact
120
atgaactgta agtccagtc aagtgttttc tacagttaa atcagaggaa ttatttggcc
180
tggtatcagc agaaaccagg gcagtcctcc aaattgctga tctactgggc atctactagg
240
gaatctgggtg tccctgatcg cttcacaggc agtggatccg ggacagactt tactcttacc
300
atcagcagtg tacatactga agacctggca gtttattact gtcataaatt cctctcttcg
360
tggacgttcg gtggaggcac caagctggaa atcaaaaggcg gtggtggttc ggggtgggtg
420
ggttcgggtg gcggcggtc ttctcaggtc caactgcagc agcctggggc tgaactgggtg
480
aagcctggga cttcagtgaa gctgtcctgc aaggcctctg gctacacctt caccaactac
540
tggatggctt ggggtgaagca gacgcctgga gaagcccttg agtggattgg agaaaattatt
600
cctagcaacg gtcgtactaa atacaatgag aagttaaga gcaaggccac actgactgca
660
gacaaatcct cccgcacagc ctacatgcaa ctcagcagcc tggcatctga ggactctgcg
720
gtctattatt gtgaagaga gatgtccatt attactacgg tactgactcc cggtttgctt
780
actggggcca agggactctg gtcactgtct ctgcagcctg atca
824
```

```
<210> 11
<211> 266
<212> PRT
<213> Mus musculus
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<220>
<221> INIT_MET
<222> (1)..(1)
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<220>
<221> SIGNAL
<222> (1)..(2)
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<220>
<221> DOMAIN
<222> (23)..(128)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20
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```
<220>
<221> SITE
<222> (129)..(144)
<223> ASP-(GLY3SER)-(GLY4SER)2-SER LINKER PEPTIDE
```

```
<220>
<221> DOMAIN
<222> (145)..(266)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20
```

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<400> 11
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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
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49076.000004pct2_10.207.655 Seq List Text 07.24.03.txt

50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Thr Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Val Thr Val Ser Asp
260 265

<210> 12
<211> 271
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)..(271)
<223> MOUSE ANTI-HUMAN CD19 SCFV

<400> 12

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
20 25 30
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
35 40 45
Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser
65 70 75 80
Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95
Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys
100 105 110
Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125
Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
130 135 140
Gly Ser Ser Gln Val Gln Leu Gln Ser Gly Ala Glu Leu Val Arg
145 150 155 160
Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe
165 170 175
Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
180 185 190
Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn
195 200 205
Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser
210 215 220
Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
225 230 235 240
Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr
245 250 255
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
260 265 270

<210> 13
<211> 259
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)..(259)
<223> MOUSE ANTI-HUMAN CD37 SCFV

<400> 13

Met Val Ser Thr Ala Gln Phe Leu Gly Leu Leu Leu Leu Trp Leu Thr
1 5 10 15
Gly Gly Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
20 25 30
Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Thr Ser Glu Asn
35 40 45
Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro
50 55 60
gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser
65 70 75 80
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser
85 90 95
Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser
100 105 110
Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys Gly
115 120 125
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ala
130 135 140
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser
145 150 155 160
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn
165 170 175
Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly
180 185 190
Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys
195 200 205
Gly Lys Ala Thr Leu Thr Val Asp Gly Ser Ser Ser Thr Ala Tyr Met
210 215 220
Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
225 230 235 240
Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
245 250 255
Val Ser Ser

<210> 14
<211> 272
<212> PRT
<213> Mus musculus

<220>
<221> SITE
<222> (1)..(272)
<223> MOUSE ANTI-HUMAN CD22 SCFV

<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

Val	20	Ser	35	Ala	40	Gly	45	Glu	50	Lys	55	Val	60	Thr	65	Met	70	Asn	75	Cys	80	Lys	85	Ser	90	Gln	95	Ser	100
Val	105	Phe	110	Tyr	115	Ser	120	Ser	125	Asn	130	Gln	135	Arg	140	Asn	145	Tyr	150	Leu	155	Ala	160	Trp	165	Tyr	170	Gln	175
Lys	180	Pro	185	Gly	190	Gln	195	Ser	200	Pro	205	Lys	210	Leu	215	Leu	220	Ile	225	Tyr	230	Trp	235	Ala	Ser	240	Thr	245	Arg
Glu	250	Ser	255	Gly	260	Val	265	Pro	270	Asp	275	Arg	Phe	280	Thr	285	Gly	290	Ser	295	Gly	Ser	Gly	Ser	Gly	300	Thr	305	Asp
Phe	310	Thr	315	Leu	320	Thr	325	Ile	330	Ser	335	Ser	340	Val	345	His	350	Thr	355	Glu	360	Asp	365	Leu	370	Ala	375	Val	380
Tyr	385	Cys	390	His	395	Gln	400	Phe	405	Leu	410	Ser	415	Ser	420	Trp	425	Thr	430	Phe	435	Gly	440	Gly	445	Thr	450	Lys	455
Leu	460	Glu	465	Ile	470	Lys	475	Gly	480	Gly	485	Gly	490	Ser	495	Gly	500	Gly	505	Gly	510	Pro	515	Gly	520	Ala	525	Glu	530
Gly	535	Thr	540	Ser	545	Ser	550	Gln	555	Val	560	Gln	565	Leu	570	Gln	575	Gln	580	Pro	585	Gly	590	Ala	595	Glu	600	Val	605
Lys	610	Pro	615	Gly	620	Thr	625	Ser	630	Val	635	Lys	640	Leu	645	Ser	650	Cys	655	Lys	660	Ala	665	Ser	670	Gly	675	Tyr	680
Phe	685	Thr	690	Asn	695	Tyr	700	Trp	705	Met	710	Val	715	Trp	720	Val	725	Lys	730	Gln	735	Thr	740	Pro	745	Gly	750	Thr	755
Leu	760	Glu	765	Trp	770	Ile	775	Gly	780	Glu	785	Ile	790	Ile	795	Pro	800	Ser	805	Asn	810	Gly	815	Arg	820	Lys	825	Tyr	830
Asn	835	Glu	840	Lys	845	Phe	850	Lys	855	Ser	860	Lys	865	Ala	870	Thr	875	Leu	880	Thr	885	Ala	890	Asp	895	Lys	900	Ser	905
Arg	910	Thr	915	Ala	920	Tyr	925	Met	930	Gln	935	Leu	940	Ser	945	Ser	950	Leu	955	Ala	960	Ser	Glu	965	Asp	970	Ser	975	Ala
Val	980	Tyr	985	Tyr	990	Cys	995	Ala	1000	Arg	1005	Glu	1010	Met	1015	Ser	1020	Ile	1025	Thr	1030	Thr	1035	Val	1040	Leu	1045	Thr	1050
Pro	1055	Gly	1060	Leu	1065	Leu	1070	Thr	1075	Gly	1080	Ala	1085	Lys	1090	Gly	1095	Leu	1100	Trp	1105	Ser	1110	Leu	1115	Ser	1120	Leu	1125

<210> 15
 <211> 499
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN
 <220>
 <221> SITE
 <222> (1)..(265)
 <223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7
 <220>
 <221> DOMAIN
 <222> (266)..(499)
 <223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

<400> 15

Met	1	Asp	5	Phe	10	Gln	15	Val	20	Gln	25	Ile	30	Phe	35	Ser	40	Leu	45	Leu	50	Ile	55	Ser	60	Ala	65	Ser	70
Val	75	Ile	80	Ile	85	Ala	90	Arg	95	Gly	100	Gln	105	Ile	110	Val	115	Leu	120	Ser	125	Gln	130	Ser	135	Pro	140	Ala	145
Leu	150	Ser	155	Ala	160	Ser	165	Pro	170	Gly	175	Glu	180	Lys	185	Val	190	Thr	195	Met	200	Thr	205	Cys	210	Arg	215	Ala	220
Ser	225	Ser	230	Val	235	Ser	240	Tyr	245	Met	250	His	255	Trp	260	Tyr	265	Gln	270	Gln	275	Lys	280	Pro	285	Gly	290	Ser	295
Pro	300	Lys	305	Pro	310	Trp	315	Ile	320	Tyr	325	Ala	330	Pro	335	Ser	340	Asn	345	Leu	350	Ala	355	Ser	360	Gly	365	Val	370
Ala	375	Arg	380	Phe	385	Ser	390	Gly	395	Ser	400	Gly	405	Ser	410	Thr	415	Ser	420	Tyr	425	Ser	430	Leu	435	Thr	440	Ile	445
Ser	450	Arg	455	Val	460	Glu	465	Ala	470	Glu	475	Asp	480	Ala	485	Ala	490	Thr	495	Tyr	500	Tyr	Cys	505	Gln	510	Gln	515	Trp
Ser	520	Phe	525	Asn	530	Pro	535	Pro	540	Thr	545	Phe	550	Ala	555	Gly	560	Thr	565	Lys	570	Leu	575	Glu	580	Leu	585	Lys	590

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys
 260 265 270
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 275 280 285
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 290 295 300
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 305 310 315 320
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 325 330 335
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 340 345 350
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 355 360 365
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 370 375 380
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 385 390 395 400
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 405 410 415
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 420 425 430
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Pro Pro
 435 440 445
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 450 455 460
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 465 470 475 480
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 485 490 495
 Pro Gly Lys

<210> 16
 <211> 499
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>
 <221> SITE
 <222> (1)..(265)
 <223> 2H7 SCFV TARGETED TO HUMAN CD20

<220>
 <221> DOMAIN
 <222> (265)..(499)
 <223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
 PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

<400> 16

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
130 135 140 145
Gln Ala Tyr Leu Gln Gln Ser Gly Val Ala Ser Gly Thr Phe Thr Ser Tyr
150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
260 265 270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275 280 285
Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305 310 315 320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340 345 350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415 420
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
425 430 435
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
440 445 450
Val Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val
455 460 465
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
470 475 480 485
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
490 495
Pro Gly Lys

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<210> 17
<211> 499
<212> PRT

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)
CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

```

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245      250      255
Gly Thr Gly Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
260      265      270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275      280      285
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290      295      300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305      310      315      320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325      330      335
His Asn Ala Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340      345      350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355      360      365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370      375      380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385      390      395      400

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
435 440 445
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
465 470 475 480
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
485 490 495
Pro Gly Lys

<210> 18
<211> 505
<212> PRT
<213> Artificial Sequence

<220>
<223> MOUSE-HUMAN FUSION PROTEIN

<220>
<221> SITE
<222> (1)..(265)
<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>
<221> DOMAIN
<222> (266)..(288)
<223> WILD TYPE IGA HINGE

<220>
<221> DOMAIN
<222> (289)..(505)
<223> HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

<400> 18
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
130 135 140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145 150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
225 230 235
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr
260 265 270
Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys
275 280 285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
290 295 300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
305 310 315 320
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
325 330 335
Val Asp Gln Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
340 345 350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385 390 395 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
405 410 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
420 425 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
435 440 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
450 455 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475 480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys
500 505

<210> 19

<211> 234

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(234)

<223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)

WILD TYPE CH2 AND CH3 DOMAINS

ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser
1 5 10 15
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
20 25 30
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
35 40 45
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
50 55 60
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
65 70 75 80
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
85 90 95
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
100 105 110
Lys Ala Leu Pro Ala Pro Ile Glu Thr Ile Ser Lys Ala Lys Gly
115 120 125
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
130 135 140
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
145 150 155 160
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
165 170 175
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
180 185 190
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
195 200 205
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
210 215 220
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 20
<211> 240
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(23)
<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>
<221> DOMAIN
<222> (24)..(240)
<223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro
1 5 10 15
Pro Thr Pro Ser Pro Ser Cys Ala Pro Glu Leu Leu Gly Gly Pro Ser
20 25 30
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
35 40 45
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
50 55 60
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
65 70 75 80
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
85 90 95
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
100 105 110
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
115 120 125
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
130 135 140
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
145 150 155 160
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
165 170 175
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
180 185 190
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
195 200 205
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
210 215 220
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230 235 240

<210> 21
<211> 1470
<212> DNA
<213> Artificial Sequence

<220>
<223> MOUSE-HUMAN HYBRID

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<220>
<221> misc_feature
<222> (1)..(808)
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>
<221> misc_feature
<222> (814)..(1455)
<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

<400> 21
aagcttgccg ccatggattt tcaagtcgag attttcagct tcttgctaatt cagtgttcca
60
gtcataattg ccaggaggaca aattgtttctc tcccagcttc cagcaatcct gttcgtcatct
120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgactagg
180
taccagcaga agccaggatc ctcccccaaa ccttggaatt atgccccatc caactggct
240
tctggagtc cttgctcgctt cagtggcagt ggtctggga cctcttactc tctcaaatc
300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaacca
360
cccacgttcg gtgctgggac caagctggag ctgaagaatg gcggtggctc gggcggtggt
420
ggactctggag gagtggggag ctctcaggct tatctacagc agtctggggc tgagctggtg
480
aggcctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac
540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat
600
caggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta
660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg
720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cagtgtctgg
780
ggcagcagga ccacggtcac cgtctctgat ccaagaaggt tggacaagat agaagatgaa
840
aggaaatctc atgaagattt tgtattcatg aaaacgatac agagatgcaa cacaggagaa
900
agatccttat ctttactgaa ctgtgaggag attaaaagcc agtttgaagg ctttggtaag
960
gatataatgt taaacaaaga ggagacgaag aaaaaaaca gctttgaaat gcaaaaaggt
1020
gatcagatc ctcaaatgac ggcacatgac ataagtgagg ccagcagtaa aacaacatct
1080
gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggt aacctggaa
1140
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtacc
1200
ttctgttcca atcggaagac ttcgagtcaa gctccattta tagccagcct ctgcctaaag
1260
tccccgggta gattcgagag aatcttactc agagctgcaa ataccacagc ttccgccaaa
1320
ccttgcgggc aacaatccat tcacttggga ggagttatgt aattgcaacc aggtgtcttcg
1380
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cagctccttt
1440
ggcttactca aactcgagtg ataacttaga
1470

<210> 22
<211> 1290
<212> DNA
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>
<223> MOUSE-HUMAN HYBRID

<220>
<221> misc_feature
<222> (13)..(808)
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>
<221> misc_feature
<222> (814)..(1275)
<223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22
aagcttgccg ccattgattt tcaagtgcag attttcagct tctgctaatt cagtgttca
60
gtcataattg ccaggaggaca aattgttctc tccagctctc cagcaatcct gtctgcattc
120
ccaggggaga aggtcacaat gacttgagg gccagctcaa gtgtaagtta catgactagg
180
taccagcaga agccaggatc ctcccccaaa ccttgattt atgccccatc caactgggt
240
tctggagtcg ctgctcgctt cagtggcagt ggtctggga cctcttactc tctcacaatc
300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca
360
cccagcttg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtgg
420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt
480
aggctgggg cctcagtgaa gatgtcctgc aagccttctg gctacacatt taccagttac
540
aatatgcact gggtaaaaga gacacctaga caggccttg aatggattgg agctatttat
600
ccaggaaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actgactgta
660
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgag
720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg
780
ggcacaggga ccacgggtcac cgtctctgat ccagaaaaca gctttgaaat gcaaaaagg
840
gatcagaatc ctcaaattgc ggcacatgct ataagtgagg ccagcagtaa aacaacatct
900
gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggg aacctggaa
960
aatgggaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcaac
1020
ttctgttcca atcggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag
1080
tccccggga gattcgagag aatcttactc agagctgcaa ataccacag ttccgcca
1140
ccttgcgggc aacaatccat tcaactggga ggagtatttg aattgcaacc aggtgcttcg
1200
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cagctcctt
1260
ggcttactca aactcgagtg ataactcaga
1290

<210> 23
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 23

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
gtcaagcttg ccgccatgga ttttcaagtg cagatttttc agc
43

<210> 24
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 24
gtcgtcgagc tcccacctcc tccagatcca ccaccgccc agccaccgcc accttcagc
60
tccagcttg tccc
74

<210> 25
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 25
gctgctgagc tctcaggctt atctacagca agtctgg
37

<210> 26
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 26
gttgctgat cagagacggt gaccgtggtc cc
32

<210> 27
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 27
gttgctggat ccagaaaaca gctttgaaat gcaa
34

<210> 28
<211> 44
<212> DNA
<213> Artificial Sequence

<220>

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> OLIGONUCLEOTIDE

<400> 28
gttgtttcta gattatcact cgagtttgag taagccaaag gacg
44

<210> 29
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 29
gttgtcggat ccaagaaggt tggacaagat agaag
35

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 30
gtctatataa gcagagctct ggc
23

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 31
cgaggctgat cagcgagctc tagca
25

<210> 32
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> OLIGONUCLEOTIDE

<400> 32
ccgcaatttg aggattctga tcacc
25

<210> 33
<211> 482
<212> PRT
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>
<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>
<221> SITE
<222> (1)..(266)
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>
<221> DOMAIN
<222> (268)..(481)
<223> EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

<400> 33

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Ser Gln Ser Pro Ala Ile
20
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245      250      255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
260      265      270
Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
275      280      285
Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
290      295      300
Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
305      310      315
Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
320      325      330
Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
335      340      345
Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Thr Met
350      355      360
Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
365      370      375
Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
380      385      390      395
Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
400      405      410      415
Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
420      425      430

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49076.000004pct2 10.207.655 seq List Text 07.24.03.txt
 Ser Ser Ala Lys Pro Cys Gly Gln Ser Ile His Leu Gly Gly Val
 435 440 445
 Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
 450 455 460
 Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
 465 470 475 480
 Leu Glu

<210> 34
 <211> 422
 <212> PRT
 <213> Artificial sequence

<220>
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>
 <221> SITE
 <222> (1)..(266)
 <223> MOUSE ANTI-HUMAN SCFV

<220>
 <221> DOMAIN
 <222> (268)..(421)
 <223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu
 260 265 270
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
 275 280 285
 Glu Ala Ser Ser Lys Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
 290 295 300

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
305 310 315 320
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
325 330 335
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
340 345 350
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
355 360 365
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
370 375 380
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
385 390 395
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
405 410 415
Gly Leu Leu Lys Leu Glu
420

<210> 35
<211> 63
<212> DNA
<213> Homo sapiens

<220>
<221> N_region
<222> (1)..(63)
<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

<400> 35
ccagttccct caactccacc taccccatct ccttcaactc cacctacccc atctccctca
60
tgc
63

<210> 36
<211> 21
<212> PRT
<213> Homo sapiens

<400> 36

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<210> 37
<211> 763
<212> DNA
<213> Homo sapiens

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<223> BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

<220>
<221> N_region
<222> (8)..(752)
<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

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 763

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 <212> PRT
 <213> Homo sapiens

<220>
 <221> DOMAIN
 <222> (3)..(250)
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 ATTACHMENT TO SECRETORY COMPONENT

<400> 38

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			20					25					30		
Pro	Ala	Leu	Glu	Asp	Leu	Leu	Leu	Gly	Ser	Glu	Ala	Ile	Leu	Thr	Cys
			35					40					45		
Thr	Leu	Thr	Gly	Leu	Arg	Asp	Ala	Ser	Gly	Val	Thr	Phe	Thr	Trp	Thr
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				70					75					80	
Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala	Glu	Pro
			85						90					95	
Trp	Asn	His	Gly	Lys	Thr	Phe	Thr	Cys	Thr	Ala	Ala	Tyr	Pro	Glu	Ser
			100					105					110		
Lys	Thr	Pro	Leu	Thr	Ala	Thr	Leu	Ser	Lys	Ser	Gly	Asn	Thr	Phe	Arg
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Pro	Glu	Val	His	Leu	Leu	Pro	Pro	Pro	Ser	Glu	Glu	Leu	Ala	Leu	Asn
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Glu	Leu	Val	Thr	Leu	Thr	Cys	Leu	Ala	Arg	Gly	Phe	Ser	Pro	Lys	Asp
			145				150			155				160	
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			165					170					175		
Tyr	Leu	Thr	Trp	Ala	Ser	Arg	Gln	Glu	Pro	Ser	Gln	Gly	Thr	Thr	Thr
			180				185						190		
Phe	Ala	Val	Thr	Ser	Ile	Leu	Arg	Val	Ala	Ala	Glu	Asp	Trp	Lys	Lys
			195				200					205			
Gly	Asp	Thr	Phe	Ser	Cys	Met	Val	Gly	His	Glu	Ala	Leu	Pro	Leu	Ala
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245 250

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<213> Artificial Sequence

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<212> PRT
<213> Artificial Sequence

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<223> Sequence contained in the core hinge region of human IgG1.

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<212> PRT
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Pro Thr Ser Pro Val Pro Gln Asp
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<210> 42
<211> 1593
<212> DNA
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 35 40 45
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 50 55 60
 Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
 65 70 75 80
 Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
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 Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
 100 105 110
 Tyr Gln Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
 115 120 125
 Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
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 His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
 145 150 155
 Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
 160 165 170
 Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
 175 180 185
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 190 195 200 205
 Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
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 Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
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 Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
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 275 280 285
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 325 330 335
 Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
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 355 360 365
 Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
 370 375 380
 Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
 385 390 395 400
 Ile Thr Gly Leu Ser
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<211> 4473
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<212> PRT
<213> Homo sapiens

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35 40 45
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50 55 60
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65 70 75 80
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
85 90 95
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
100 105 110
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
115 120 125
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130 135 140
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145 150 155
Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
160 165 170
Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
175 180 185 190
His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
195 200 205
Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
210 215 220
Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225 230 235 240
Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
245 250 255
His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
260 265 270
Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
275 280 285
Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
290 295 300
Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305 310 315 320
Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
325 330 335
Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
340 345 350
Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
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420 425 430
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435 440 445
Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
450 455 460
Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465 470 475 480
Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
485 490 495
Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
500 505 510
Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
515 520 525
Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
530 535 540
Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545 550 555 560
Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
555 560 565
Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Thr Lys Asp
565 570 575
Pro Pro Phe Cys Val Ala Arg Cys Ser Gly Val Lys Pro Asp Leu
580 585 590
Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
595 600 605
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610 615 620
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625 630 635 640
Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
645 650 655 660
Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
665 670 675 680
Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
685 690 695 700
Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
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Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
725 730 735
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
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755 760 765 770
Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
775 780 785
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790 795 800
Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
805 810 815
Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
820 825 830
Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
835 840 845
Arg Asn Val Leu Val Lys Ser Asn His Val Lys Ile Thr Asp Phe
850 855 860
Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865 870 875 880
Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
885 890 895
Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
900 905 910
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995 1000
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275 285
Ala Thr Cys Val Lys Lys Cys 295 Pro Arg Asn Tyr Val Val Thr Asp His
290 300
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305 315
Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
320 335
Cys Asn Gly Ile Gly Ile Gly Glu Phe 345 Lys Asp Ser Leu Ser Ile Asn
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Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
355 365
Leu His Ile Leu Pro Val Ala 375 Phe Arg Gly Asp Ser 380 Phe Thr His Thr
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<213> Homo sapiens

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Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
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Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
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Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
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<211> 3166
<212> DNA
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 <213> Homo sapiens

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 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
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 Met Arg Cys Gly Gly Cys Ser Asn Asp Gln Gly Leu Glu Cys Val Pro
 85 90 95
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
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 Gln Gly Gln His Ile Gly Glu Met Ser His Gln His Asn Lys Cys
 115 120 125
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly
 130 135 140
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
 145 150 155 160
 Cys Lys Cys Ser Cys Lys Asn Thr His Ser Arg Cys Lys Ala Arg Gln

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 <212> PRT
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 35 40 45
 Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe
 50 55 60
 Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly
 65 70 75 80
 Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys
 85 90 95
 Phe Arg Ser Cys Asp Leu Arg Arg Leu Met Tyr Cys Ala Pro Leu
 100 105 110
 Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp
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aaatagtatt	gtgggtttttg	taggttttta	aaataacctt	ttttggggag	agaattgtcc	4980
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<210> 63
<211> 933
<212> PRT
<213> Homo sapiens

<400> 63
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Ala Gly Pro Phe Pro Gly Thr Ser Asp Thr Leu Pro Glu Val
35 40 45
Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60
Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80
Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95
Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp

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100 105 110
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115 120 125
Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140
Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160
Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175
Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190
Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205
Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu
210 215 220
Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240
Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Ala Ala Ala Cys
245 250 255
Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270
Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285
Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300
His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320
Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335
Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350
Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365
Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380
Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400
Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415
Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430
Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445
Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460
Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Cys
465 470 475 480
Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495
Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510
Pro Ala Leu Gly Leu Asn Gly Leu Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
515 520 525
Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540
Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560
Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575
Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590
Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605
Cys Ile Val Asp Lys Ile Arg Gln Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620
Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
625 630 635 640
Lys Phe Asn Lys Val Arg Val Val Arg Ala Leu Asp Ala Val Ala Leu
645 650 655

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675 680 685
Asn Leu Leu Met Ser Ile Gln Pro Asp Val Ile Tyr Ala Gly His Asp
690 695 700
Asn Thr Lys Pro Asp Thr Ser Ser Leu Leu Thr Ser Leu Asn Gln
705 710 715
Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
720 725 730
Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
735 740 745
Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr
750 755 760
Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu
765 770 775
Asn Gln Gln Arg Met Lys Gln Ser Ser Phe Tyr Ser Leu Cys Leu Thr
780 785 790 795
Met Trp Gln Ile Pro Gln Gln Phe Val Lys Leu Gln Val Ser Gln Glu
800 805 810 815
Glu Phe Leu Cys Met Lys Val Leu Leu Leu Asn Thr Ile Pro Leu
820 825 830
Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr
835 840 845
Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val
850 855 860
Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu
865 870 875 880
His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile
885 890 895
Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val
900 905 910
Ile Ala Ala Gln Leu Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu
915 920 925
Leu Phe His Lys Lys
930

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<211> 2393
<212> DNA
<213> Homo sapiens

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catattcagg tctgtcactg ctctaacagg gtttttctct gccaaagagat caaggtgaca 180
gagattctct ctgacctccc gaggaatgcc attgaaactga ggtttgtctc caccagcttt 240
cgagtcaccc aaaaagggtc attttcagga tttggggacc tggagaaaat agagattctc 300
cagaatgatg tctttggagg gatagaggca gatgtgttct ccaaccttcc caaattacat 360
gaaattagaa ttgaaaaggc caacaactct ctctacatca cccctgaggc ctccagaac 420
cttcccaacc ttcaatatct gttaatatcc aacacaggtta ttaagcactt tccagatgtt 480
cacagattcc attctctcca aaaggtttta cttgacattc aagataacat aaactccac 540
acaattgaaa gaaattcttt cgtggggcgt agcttttgaaa gtgtgattct atggtgaa 600
aagaattggga ttcaagaagt acacaactgt gcattccaatg gaaccacact agatgcagt 660
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 acaagagact gcagagtctt ctacacattt catctaatat aatattctgt gcataccttt 2280
 aaggttaatt ggtcaggaaac tattaatctc atgtgatata ttaggaaagt gaattattag 2340
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ile Glu Leu Arg Phe Val Leu Thr Lys Leu Arg Val Ile Gln Lys Gly
 50 55 60
 Ala Phe Ser Gly Phe Gly Asp Leu Glu Lys Ile Glu Ile Ser Gln Asn
 65 70 75
 Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys
 80 85 90
 Leu His Glu Ile Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Thr
 100 105 110
 Pro Glu Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser
 115 120 125
 Asn Thr Gly Ile Lys His Leu Pro Asp Val His Lys Ile His Ser Leu
 130 135 140
 Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Thr Ile
 145 150 155
 Glu Arg Asn Ser Phe Val Gly Leu Ser Phe Glu Ser Val Ile Leu Trp
 160 165 170
 Leu Asn Lys Asn Gly Ile Gln Glu Ile His Asn Cys Ala Phe Asn Gly
 180 185 190
 Thr Gln Leu Asp Ala Val Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu
 195 200 205
 Leu Pro Asn Asp Val Phe His Gly Ala Ser Gly Pro Val Ile Leu Asp
 210 215 220
 Ile Ser Arg Thr Arg Ile His Ser Leu Pro Ser Tyr Gly Leu Glu Asn
 225 230 235
 Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Asn Leu Lys Lys Leu Pro
 240 245 250
 Thr Leu Glu Lys Leu Val Ala Leu Met Glu Ala Ser Leu Thr Tyr Pro
 255 260 265
 Ser His Cys Cys Ala Phe Ala Asn Trp Arg Arg Gln Ile Ser Glu Leu
 270 275 280
 His Pro Ile Cys Asn Lys Ser Ile Leu Arg Gln Glu Val Asp Tyr Met
 285 290 300
 Thr Gln Ala Arg Gly Gln Arg Ser Ser Leu Ala Glu Asp Asn Glu Ser
 305 310 315
 Ser Tyr Ser Arg Gly Phe Asp Met Thr Tyr Thr Glu Phe Asp Tyr Asp
 320 325 330
 Leu Cys Asn Glu Val Val Asp Val Thr Cys Ser Pro Lys Pro Asp Ala
 335 340 345
 Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Asn Ile Leu Arg Val Leu
 350 355 360
 Ile Trp Phe Ile Ser Ile Leu Ala Ile Thr Gly Asn Ile Ile Val Leu

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370 375 380
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405 410 415
Leu Ile Ala Ser Val Asp Ile His Thr Lys Ser Gln Tyr His Asn Tyr
420 425 430
Ala Ile Asp Trp Gln Thr Gly Ala Gly Cys Asp Ala Ala Gly Phe Phe
435 440 445
Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Ala Ile Thr
450 455 460
Leu Glu Arg Trp His Thr Ile Thr His Ala Met Gln Leu Asp Cys Lys
465 470 475 480
Val Gln Leu Arg His Ala Ala Ser Val Met Val Met Gly Trp Ile Phe
485 490 495
Ala Phe Ala Ala Ala Leu Phe Pro Ile Phe Gly Ile Ser Ser Tyr Met
500 505 510
Lys Val Ser Ile Cys Leu Pro Met Asp Ile Asp Ser Pro Leu Ser Gln
515 520 525
Leu Tyr Val Met Ser Leu Leu Val Leu Asn Val Leu Ala Phe Val Val
530 535 540
Ile Cys Gly Cys Tyr Ile His Ile Tyr Leu Thr Val Arg Asn Pro Asn
545 550 555
Ile Val Ser Ser Ser Asp Thr Arg Ile Ala Lys Arg Met Ala Met
565 570 575
Leu Ile Phe Thr Asp Phe Leu Cys Met Ala Pro Ile Ser Phe Phe Ala
580 585 590
Ile Ser Ala Ser Leu Lys Val Pro Leu Ile Thr Val Ser Lys Ala Lys
595 600 605
Ile Leu Leu Val Leu Phe His Pro Ile Asn Ser Cys Ala Asn Pro Phe
610 615 620
Leu Tyr Ala Ile Phe Thr Lys Asn Phe Arg Arg Asp Phe Phe Ile Leu
625 630 635
Leu Ser Lys Cys Gly Cys Tyr Glu Met Gln Ala Gln Ile Tyr Arg Thr
645 650 655
Glu Thr Ser Ser Thr Val His Asn Thr His Pro Arg Asn Gly His Cys
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Ser Ser Ala Pro Arg Val Thr Ser Gly Ser Thr Tyr Ile Leu Val Pro
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Leu Ser His Leu Ala Gln Asn
690 695

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<212> DNA
<213> Homo sapiens

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ggcccttcag ggcacaaaaa aagatgccac tcttagatgg gccccagcta ggtggctgag 180
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cagcagttct gaagagatag tgcacagccc tccctcgcca cccctctcac ccgcagctc 480
caagctctgc ttgtctgtc aggacaagtc ctacggctac cactatgggg tcagcgctg 540
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ccgggacaag aactgcatca tcaacaaggt gaccccgaac cgctgccact actgcgcact 660
gcagaagtgc ttggaagtg gcatgtccaa ggagtctgtg agaaacgacc gaacacagaa 720
gaagaaggag tgcgccaaag ccgagtgctc tgagagctac acgtgcagcc cggaggtggg 780
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<210> 67
<211> 432
<212> PRT
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<400> 67
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35 40 45
Pro Pro Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys
50 55 60
Ser Ser Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly
65 70 75 80
Phe Phe Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg
85 90 95
Asp Lys Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr
100 105 110
Cys Arg Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val
115 120 125
Arg Asn Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys Pro Glu Cys
130 135 140
Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys
145 150 155 160
Val Arg Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly
165 170 175
Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile
180 185 190
Asp Leu Trp Asp Lys Phe Ser Glu Leu Ser Thr Lys Cys Ile Ile Lys
195 200 205
Thr Val Glu Phe Ala Lys Gln Leu Pro Gly Phe Thr Thr Leu Thr Ile
210 215 220
Ala Asp Gln Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Ile
225 230 235 240
Leu Arg Ile Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe
245 250 255
Ser Asp Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe
260 265 270
Gly Pro Leu Thr Asp Leu Val Phe Ala Phe Ala Asn Gln Leu Leu Pro
275 280 285
Leu Glu Met Asp Asp Ala Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu
290 295 300
Ile Cys Gly Asp Arg Gln Asp Leu Gln Pro Asp Arg Val Asp Met
305 310 315 320
Leu Gln Glu Pro Leu Leu Glu Ala Leu Lys Val Tyr Val Arg Lys Arg
325 330 335 340
Arg Pro Ser Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr
345 350 355
Asp Leu Arg Ser Ile Ser Ala Lys Gly Ala Glu Arg Val Ile Thr Leu
360 365 370
Lys Met Glu Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu
375 380 385
Glu Asn Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly

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385 390 395
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Ser Leu Ser Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro
420 425 430

<210> 68
<211> 3576
<212> DNA
<213> Mus musculus

<400> 68
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cttccatgtt ttgctgtcc agggcctttc tegtgtttct ttctctcttc tggcgtgtac 180
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atcaagttca ggtacgttct ggatttgact tggggaggga atggtcagtc tctgtactat 2820
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cagcttgcca cactactatg ggggtttacc ttctgtttac ttctggcgc aggaagtggga 3120
aatccactcc ctttggggag ttccctgacc accgcttttc ttcttagtga atagataga 3180
gttccctccc cctggccagt ccggccggg ggtaccagcg tggggcattg cctgtctgtg 3240
gtgtgtctgt atttttgggt ctttggctat cgtctatttc ctgcccgtg taagtctcaa 3300
gcttctgctg gcgctgtgtg ccttggtaa atgggaaggg atgggccaat ccaatctctc 3360

http://www.uspto.gov/patent

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gtctccctag gcagttgtgcc agtgcgcgcg aaagagctat gggcagctgg acatctttcc 3420
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cgtgccctt ggcagtacca agcgtcagcc ctatgaggag gtaaaagtga tcccgagaa 3540
gcttgggcca tcgacctggg cagggtgggg ccttct 3576

<210> 69
<211> 630
<212> PRT
<213> MUS musculus

<400> 69
Met Thr Pro Gly Ile Arg Ala Pro Phe Phe Leu Leu Leu Leu Ala
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Ser Leu Lys Gly Phe Leu Ala Leu Pro Ser Glu Glu Asn Ser Val Thr
20 25 30
Ser Ser Gln Asp Thr Ser Ser Ser Leu Ala Ser Thr Thr Pro Val
35 40 45
His Ser Ser Asn Ser Asp Pro Ala Thr Arg Pro Gly Asp Ser Thr
50 55 60
Ser Ser Pro Val Gln Ser Ser Thr Ser Ser Pro Ala Thr Arg Ala Pro
65 70 75 80
Glu Asp Ser Thr Ser Thr Ala Val Leu Ser Gly Thr Ser Ser Pro Ala
85 90 95
Thr Thr Ala Pro Val Asn Ser Ala Ser Pro Val Ala His Gly Asp
100 105 110
Thr Ser Ser Pro Ala Thr Ser Pro Lys Asp Ser Asn Ser Ser Pro
115 120 125
Val Val His Ser Gly Thr Ser Ala Ala Thr Thr Ala Pro Val Asp
130 135 140
Ser Thr Ser Ser Pro Val Val His Gly Gly Thr Ser Ser Pro Ala Thr
145 150 155 160
Ser Pro Pro Gly Asp Ser Thr Ser Ser Pro Asp His Ser Ser Thr Ser
165 170 175
Ser Pro Ala Thr Arg Ala Pro Glu Asp Ser Thr Ser Thr Ala Val Leu
180 185 190
Ser Gly Thr Ser Ser Pro Ala Thr Thr Ala Pro Val Asp Ser Thr Ser
195 200 205
Ser Pro Val Ala His Asp Asp Thr Ser Ser Pro Ala Thr Ser Leu Ser
210 215 220
Glu Asp Ser Ala Ser Ser Pro Val Ala His Gly Gly Thr Ser Ser Pro
225 230 235 240
Ala Thr Ser Pro Leu Arg Asp Ser Thr Ser Ser Pro Val His Ser Ser
245 250 255
Ala Ser Ile Gln Asn Ile Lys Thr Thr Ser Asp Leu Ala Ser Thr Pro
260 265 270
Asp His Asn Gly Thr Ser Val Thr Thr Ser Ser Ala Leu Gly Ser
275 280 285
Ala Thr Ser Pro Asp His Ser Gly Thr Ser Thr Thr Thr Asn Ser Ser
290 295 300
Glu Ser Val Leu Ala Thr Thr Pro Val Tyr Ser Ser Met Pro Phe Ser
305 310 315 320
Thr Thr Lys Val Thr Ser Gly Ser Ala Ile Ile Pro Asp His Asn Gly
325 330 335
Ser Ser Val Leu Pro Thr Ser Ser Val Leu Gly Ser Ala Thr Ser Leu
340 345 350
Val Tyr Asn Thr Ser Ala Ile Ala Thr Thr pro Val Ser Gly Thr
355 360 365
Gln Pro Ser Val Pro Ser Gln Tyr Pro Val Ser Pro Thr Met Ala Thr
370 375 380
Thr Ser Ser His Ser Thr Ile Ala Ser Ser Tyr Tyr Ser Thr Val
385 390 395 400
Pro Phe Ser Thr Phe Ser Ser Asn Ser Ser Pro Gln Leu Ser Val Gly
405 410 415
Val Ser Phe Phe Phe Leu Phe Phe Tyr Ile Gln Asn His Pro Phe Asn
420 425 430 435
Ser Ser Leu Glu Asp Pro Ser Ser Asn Tyr Tyr Gln Glu Leu Lys Arg
440 445 450
Asn Ile Ser Gly Leu Phe Leu Gln Ile Phe Asn Gly Asp Phe Leu Gly
455 460

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 Ile Ser Ile Lys Phe Arg Ser Gly Ser Val Val Val Glu Ser Thr
 465 470 475 480
 Val Val Phe Arg Glu Gly Thr Phe Ser Ala Ser Asp Val Lys Ser Thr
 485 490 495
 Leu Ile Gln His Lys Lys Glu Ala Asp Ser Tyr Asn Leu Thr Ile Ser
 500 510
 Glu Val Lys Val Asn Glu Met Gln Phe Pro Pro Ser Ala Gln Ser Arg
 515 525
 Pro Gly Val Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Ile
 530 540
 Leu Val Ala Leu Ala Ile Val Tyr Phe Leu Ala Leu Ala Val Cys Gln
 545 555 560
 Cys Arg Arg Lys Ser Tyr Gly Gln Leu Asp Ile Phe Pro Thr Gln Asp
 565 570 575
 Thr Tyr His Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg
 580 585 590
 Tyr Val Pro Pro Gly Ser Thr Lys Arg Gln Pro Tyr Glu Glu Val Ser
 595 605
 Ala Gly Asn Gly Ser Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Val
 610 620
 Thr Thr Ser Ala Asn Leu
 625 630

<210> 70
 <211> 755
 <212> DNA
 <213> Homo sapiens

<400> 70
 ctctgtgggacc ctgaccttct ctctgagagc cgggcagagc ctcaggagcc atgcaggccg 60
 aaggccggggc cacagggggt tcgacggggc atgctgatgg ccacaggagcc cctggcattc 120
 ctgatggccc agggggcaat gctggcggcc caggagagggc ggggtgccag gccgcgcagag 180
 gtccccgggg cgacaggggca gcaaggccct cggggccggg aggaggccgc ccgggggggtc 240
 cgcatggcgg cgcggtctca gggctgaatg gatgctgcag atgcggggcc agggggggcgg 300
 agagccgcct gcttgagttc tacctgcgca tgcctttcgc gacacccatg gaagcagagc 360
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 aggagttcac tggctcgggc aacatactga ctatccgact gactgtctga gaccaccagc 480
 aactgcagct ctccatcagc tccgtcttcc agcagcttcc cctagttagt tggattccgc 540
 agtgccttct gccctgtgtt ttggctcagc ctccctcagg cgagaggccg taagccacgc 600
 ctggcgcccc ttccatagtc atgcctcttc ccctagggaa tggctccagc acgagtgggc 660
 agttcattgt gggggcctga ttgtttgtcg ctggaggagg acggcttaca tgttgttttc 720
 ttagaaaaat aaactcgagc tacgaaaaa aaaaa 755

<210> 71
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 71
 Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
 1 5 10 15
 Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
 20 25 30
 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
 35 40 45
 Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Ala Pro Arg Gly Pro
 50 55 60
 His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
 65 70 75 80
 Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
 85 90 95
 Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
 100 105 110
 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
 115 120 125
 Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Ser His Arg Gln
 130 135 140
 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met

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165 170 175

Gly Gln Arg
Arg

<210> 72
<211> 1524
<212> DNA
<213> Homo sapiens

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gagaagatgc tcacttcacg tatgtgttacc ccaagaagg gacgcgccac tcttacacca 120
cgcgtaaga ggcgcgtggg atcggcaccc tgacagtgat cctggggagc ttactgtcca 180
tcggctgtgt gattgtttaga agacgaaatg gatacagagc ctgtatggat aaaagtcttc 240
atgtgtggcac tcaatgtgcc ttaacaagaa gatgcccaaga agaagggttt gatcatcggg 300
acagcaaaagt gtctcttcaa gagaaaaact gtgaacctgt ggttcccaat gctccacctg 360
cttatgagaa actctctgca gaacagtcac caccacctta ttcaccttaa gagccagcga 420
gacacctgag acatgctgaa attatttctc tcacactttt gcttgaattt aatacagaca 480
tctaattgtc tccttgggaa tgggtgtagga aaaaatgcaag ccactctcaa taataagtca 540
gtgttaaaat tttagtaggt cgctagcag tactaatcat gtgaggaat gatgagaat 600
atlaaatgg gaaaactcca tcaataatg ttgcaatgca tgatactat tgggccagag 660
ggaatgttag taaatccatg gtgtatttt ctgagagaca gaattcaagt gggatttctg 720
gggcaccca atttctctt acttgaatt tggctaataa caactagtc aggttttctg 780
accttgcac acatgaactg tacacagaat tgttccagta ctatggagt ctcaaaagg 840
atactttac aggttaagac aaagggttga ctggcctatt tatctgatca agaactatgc 900
agcaatgtct ctttgtgctc taaaattcta ttatactaca ataataatt gtaaatgcc 960
tatagctctt ttttttgag atggagtttc gctttgtgt cccaggctgg agtgcaattg 1020
cgcgatcttg gctcaccata acctcgcct ccagggttca agcaattctc ctgccttagc 1080
ctcttgagta ctggggatta caggcgtgag ccatatgccc tgactaattt tgtagtttta 1140
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ctgcccgcct cagctcccca aagtgtcggg attacagggc tgagccacca cgctggctg 1260
gatctctat cttaggttaag acataaacg cagcttaatt acatttcaat tcaagggtca 1320
atgctattct aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380
ataaagtaaa agctcatatg tactgcctta gtgctgatgc ctgtgtactg ctctaaatgt 1440
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aatcataaag gatcagagat tctg 1524

<210> 73
<211> 118
<212> PRT
<213> Homo sapiens

<400> 73
Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly
1 5 10 15
His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile
20 25 30
Leu Thr Val Ile Leu Gly Val Leu Leu Ile Gly Cys Trp Tyr Cys
35 40 45
Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val
50 55 60
Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp
65 70 75 80
His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
85 90 95
Val Pro Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
100 105 110
Pro Pro Pro Tyr Ser Pro
115

<210> 74
<211> 1602
<212> DNA
<213> Mus musculus

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<400> 74
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ggtgatggga gtccctcgcg ccagcttttca ggcagaggtt cctgcccaga tatctctctg 180
tccagtggac catctggacc tcagttcccc ttcaaggggg tggatgaccg tgagttctgg 240
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agaaacattt ttgatttgag tgtctccgaa aagaataagt tctttcttta ccttacttta 420
cgaacacata ctatcagctc agtctatgtc atcccacag gcactatagg ccaaatgaac 480
aatgggtcaa caccatggt taatgatgc aacatctacg acctctttgt atgagatgat 540
tactatttgt caagggaacac actgcttggg ggctctgaaa tatggaggca gattgatatt 600
gccattgaag caccagggtt tctgctctgg cacagacttt tctgtattt ttgggaacaa 660
gaaattcgag aactaactgg ggaatgaaac ttcaactgtc catactggga ttggagagat 720
gcagaaaaact gtgacatttg cacagatgag tacttgggag gtcctcacc tgaaatcct 780
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gccacgcatc ccatttttct tcttcacatt gcttttgtag acagattttt tgaacacatt 1200
tctcgaaagg accgcctctc ttggaagtt tacccagaag ccaatgcacc ttctggcgtg 1260
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agaaattata ttgagctcta cttggaacaa gccagtcgta tctggccatg gctttctggg 1440
cgagcactgg tggagctgtt tatgtctgca gctctctctg ggccttagcag taggctatgc 1500
cttcgaagaa agaagaagaa gaagcaacc aggagagaaa gcagccact cctcatggac 1560
aaagacgact accacagctt gctgtatcag agccatctgt ga 1602

<210> 75
<211> 533
<212> PRT
<213> Mus musculus

<400> 75
Met Phe Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Ile Ser
1 5 10 15
Asp Gly His Phe Pro Arg Ala Cys Ala Ser Ser Lys Asn Leu Leu Ala
20 25 30
Lys Glu Cys Cys Pro Pro Trp Ile Gly Asp Gly Ser Pro Cys Gly Gln
35 40 45
Leu Ser Gly Arg Gly Ser Cys Gln Asp Ile Leu Leu Ser Ser Ala Pro
50 55 60
Ser Gly Pro Gln Phe Pro Phe Lys Gly Val Asp Asp Arg Glu Ser Trp
65 70 75 80
Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85 90 95
Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Gly Pro Asn Cys
100 105 110
Thr Glu Lys Arg Val Leu Ile Arg Arg Asn Ile Phe Asp Leu Ser Val
115 120 125
Ser Glu Lys Asn Lys Phe Phe Ser Tyr Leu Thr Leu Ala Lys His Thr
130 135 140
Ile Ser Ser Val Tyr Val Ile Pro Thr Gly Thr Tyr Gly Gln Met Asn
145 150 155 160
Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
165 170 175
Val Trp Met His Tyr Tyr Val Ser Arg Asp Thr Leu Leu Gly Gly Ser
180 185 190
Glu Ile Trp Arg Gln Ile Asp Phe Ala His Glu Ala Pro Gly Phe Leu
195 200 205
Pro Trp His Arg Leu Phe Leu Leu Trp Glu Gln Glu Ile Arg Glu
210 215 220
Leu Thr Gly Asp Glu Asn Phe Thr Val Pro Tyr Trp Asp Trp Arg Asp
225 230 235 240
Ala Glu Asn Cys Asp Ile Cys Thr Asp Glu Tyr Leu Gly Gly Arg His
245 250 255
Pro Glu Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
260 265 270

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Gln Ile Ile Cys Ser Arg Ser Glu Glu Tyr Asn Ser His Gln Val Leu
275 280 285
Cys Asp Gly Thr Pro Glu Gly Pro Leu Leu Arg Asn Pro Gly Asn His
290 295 300
Asp Lys Ala Lys Thr Pro Arg Leu Pro Ser Ser Ala Asp Val Glu Phe
305 310 315 320
Cys Leu Ser Leu Thr Gln Tyr Glu Ser Gly Ser Met Asp Arg Thr Ala
325 330 335
Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
340 345 350
Gly Ile Ala Asp Pro Ser Gln Ser Ser Met His Asn Ala Leu His Ile
355 360 365
Phe Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
370 375 380
Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
385 390 395 400
Leu Arg Arg His Arg Pro Leu Leu Glu Val Tyr Pro Glu Ala Asn Ala
405 410 415
Pro Ile Gly Arg Asn Arg Asp Ser Tyr Met Val Pro Phe Ile Pro Leu
420 425 430
Tyr Arg Asn Gly Asp Phe Phe Ile Thr Ser Lys Asp Leu Gly Tyr Asp
435 440 445
Tyr Ser Tyr Leu Gln Glu Ser Asp Pro Gly Phe Tyr Arg Asn Tyr Ile
450 455 460
Glu Pro Tyr Leu Glu Gln Ala Ser Arg Ile Trp Pro Trp Leu Leu Gly
465 470 475 480
Ala Ala Leu Val Gly Ala Val Ile Ala Ala Leu Ser Gly Leu Ser
485 490 495
Ser Arg Leu Cys Leu Gln Lys Lys Lys Lys Lys Gln Pro Gln Glu
500 505 510
Glu Arg Gln Pro Leu Leu Met Asp Lys Asp Asp Tyr His Ser Leu Leu
515 520 525
Tyr Gln Ser His Leu
530

<210> 76
<211> 2130
<212> DNA
<213> Homo sapiens

<400> 76
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gtgatagggt ctttgcctgc tgtgggggct acaaaagtac ccagaaacca ggactggctt 120
gggtgtctcaa ggcaactcag aaccaagacc ttggaacaggc agctgtatcc agagtggaca 180
gaagccacaga gacttgactg ctggagagggt ggctcaaggt ccctcaaggt cagtaaatgt 240
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caaaaagtac tgccagatgg gcaggttatc tgggtcaaca ataccatcat caatgggaagc 360
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gatggtggac ctgcgccatc tggctcttgg tctcagaaga gaagctttgt ttatgtctgg 480
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acaggcaggg caactgtcggg cacacacacc atggaagtga ctgtctacca tcgcccgggga 600
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actccagagg ctacagggat gacacctgca gaggtatcaa ttgtgggtgt tcttggaaac 1260
acagctggac agatataaac tacagagtgg gtggagacca cagctagaga gctactatc 1320
cctgagcctg aaggtccaga tccagctcta atcattgtta cggaaagtat tacaggtttc 1380
ctggggcccc tgctggatgg tacagccacc taaggctcgg tgaagagaca agtccgctgt 1440
gatgtgtgtc tgtatcgata tggctcctt tggactcacc tggacatcgt caggtgtatt 1500
gaaagtggcg aagtcctgca ggtctggcgg tccggtgagg gggatgcatt tcttggaaac 1560
gtgtcctgcc aaggcgggct gcccaaggaa gcctgcattg agatctcatc gccagggtgc 1620

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 cagccccctg ccagcggct gtgccagcct gtgctaccga gccagcctg ccagctggtt 1680
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 accaacagcc tggcagtggt cagcaccagc cttatcatgc ctgggtcaaga agcaggcctt 1800
 gggcaggttc cgtgcatcgt gggcattctg ctgggtgtga tggctgtggt ccttcgcatct 1860
 ctgatatata ggcgcagact tatgaagcaa gacttctcgc taccccagtt gccacatagc 1920
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 cccctctcca gtgggcagca ggtctgagta cttctcatatg atgctgtgat ttctctggag 2040
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 aatactcaga gcctgaaaaa aaaaaaaaaa 2130

<210> 77
 <211> 661
 <212> PRT
 <213> Homo sapiens

<400> 77
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 Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn Gln Asp Trp
 20 25 30
 Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu
 35 40 45
 Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly
 50 55 60
 Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
 65 70 75
 Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val
 85 90 95
 Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly
 100 105 110
 Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp
 115 120 125
 Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser
 130 135 140
 Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp
 145 150 155
 Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg
 160 165 170
 Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
 175 180 185
 Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
 190 195 200
 Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Arg Ala
 205 210 215
 Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe
 220 225 230
 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu
 235 240 245
 Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu Ile Ser Arg
 250 255 260
 Ala Leu Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala
 265 270 275
 Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
 280 285 290
 Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala Glu Ala Pro
 295 300 305
 Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr
 310 315 320
 Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr Ser Val Gln
 325 330 335
 Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln Met Pro Thr
 340 345 350
 Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val
 355 360 365
 Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala Thr Gly Met
 370 375 380
 Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr Thr Ala Ala
 385 390 395
 Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
 400 405 410 415 420

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 420 425 430
 Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile Met Ser Thr Glu
 435 440 445
 Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr Ala Thr Leu
 450 455 460
 Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
 465 470 475 480
 Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala
 485 490 495
 Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu
 500 505 510
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995 1000 1005
Ile Lys Gly Thr Tyr Ala Ser Glu Val Ile Trp Asp Val Leu Ser
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Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly His
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Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
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Tyr Ser Asn Lys Thr Phe Pro Ala Phe Leu Val Tyr Ser Thr Lys Glu
305     310     315     320
Lys Cys Lys Gln Leu Tyr Asp Thr Ile Gly Lys Phe Arg Pro Glu Phe
325     330     335
Lys Cys Leu Val His Tyr Glu Glu Gly Met Leu Phe Phe Glu Thr
340     345     350
Met Thr Lys His Arg Val Ser Ala Val Lys Asn Tyr Cys Ser Lys Leu
355     360     365
Cys Ser Val Ser Phe Leu Met Cys Lys Ala Val Thr Lys Pro Met Glu
370     375     380
Cys Tyr Gln Val Val Thr Ala Ala Pro Phe Gln Leu Ile Thr Glu Asn
385     390     395     400
Lys Pro Gly Leu His Gln Phe Glu Phe Thr Asp Glu Pro Glu Glu Gln
405     410     415
Lys Ala Val Asp Trp Ile Met Val Ala Asp Phe Ala Leu Glu Asn
420     425     430
Leu Asp Asp Pro Leu Leu Ile Met Gly Tyr Tyr Leu Asp Phe Ala Lys
435     440     445
Glu Val Pro Ser Cys Ile Lys Cys Ser Lys Glu Glu Thr Arg Leu Gln
450     455     460
Ile His Trp Lys Asn His Arg Lys His Ala Glu Asn Ala Asp Leu Phe
465     470     475     480
Leu Asn Cys Lys Ala Gln Lys Thr Ile Cys Gln Gln Ala Ala Asp Gly
485     490     495
Val Leu Ala Ser Arg Arg Leu Lys Leu Val Glu Cys Thr Arg Ser Gln
500     505     510
Leu Leu Lys Glu Arg Leu Gln Gln Ser Leu Leu Arg Leu Lys Glu Leu
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 Leu Thr Glu Asn Val Pro Lys Arg Arg Asn Ile Leu Phe Arg Gly Pro
 565 570 575
 Val Asn Ser Gly Lys Thr Gly Leu Ala Ala Leu Ile Ser Leu Leu
 580 585 590
 Gly Gly Lys Ser Leu Asn Ile Asn Cys Pro Ala Asp Lys Leu Ala Phe
 595 600 605
 Glu Leu Gly Val Ala Gln Asp Gln Phe Val Val Cys Phe Glu Asp Val
 610 615 620
 Lys Gly Gln Ile Ala Leu Asn Lys Gln Leu Gln Pro Gly Met Gly Val
 625 630 635 640
 Ala Asn Leu Asp Asn Leu Arg Asp Tyr Leu Asp Gly Ser Val Lys Val
 645 650 655
 Asn Leu Glu Lys Lys His Ser Asn Lys Arg Ser Gln Leu Phe Pro Pro
 660 665 670
 Cys Val Cys Thr Met Asn Glu Tyr Leu Leu Pro Gln Thr Val Trp Ala
 675 680 685
 Arg Phe His Met Val Leu Asp Phe Thr Cys Lys Pro His Leu Ala Gln
 690 695 700
 Ser Leu Glu Lys Cys Glu Phe Leu Gln Arg Glu Arg Ile Ile Gln Ser
 705 710 715 720
 Gly Asp Thr Leu Ala Leu Leu Leu Ile Trp Asn Phe Thr Ser Asn Val
 725 730 735
 Phe Asp Pro Asp Ile Gln Gly Leu Val Lys Glu Val Arg Asp Gln Phe
 740 745 750
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 Gln Glu Gly Asp Asp Pro Leu Lys Asp Ile Cys Glu Tyr Ser
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 <213> Homo sapiens

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 cagcacatca acttggacat tcttagtttt caaatgagtg atgatattga cgtataaaaa 180
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<212> PRT

<213> Homo sapiens

<400> 91

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Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
35      40      45
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
50      55      60
Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
65      70      75
Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
85      90      95
Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
100      105      110
Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
115      120      125
Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
130      135      140
Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
145      150      155
Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
160      165      170
Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
175      180      185
Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
190      195      200
Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
205      210      215
Val Phe Val Ala Leu Leu Val Phe Thr Lys Lys Arg Lys Lys Gln
220      225      230
Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
235      240      245
Ala Thr Glu Glu Arg Gly Arg Lys Pro Gln Gln Ile Pro Ala Ser Thr
250      255      260
Pro Gln Asn Pro Ala Thr Ser Gln Arg Pro Pro Pro Pro Gly His
265      270      275
Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
280      285      290
Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
295      300      305
His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
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340      345      350
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<211> 2026

<212> DNA

<213> Homo sapiens

<400> 92

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 35 40 45
 Glu Val Tyr Leu Lys Asp Gly Trp His Met Val Cys Ser Gln Ser Trp
 50 55 60
 Gly Arg Ser Ser Lys Gln Trp Glu Asp Pro Ser Gln Ala Ser Lys Val
 65 70 75 80
 Cys Gln Arg Leu Asn Cys Gly Val Pro Leu Ser Leu Gly Pro Phe Leu
 85 90 95
 Val Thr Tyr Thr Pro Gln Ser Ser Ile Ile Cys Tyr Gly Gln Leu Gly
 100 105
 Ser Phe Ser Asn Cys Ser His Ser Arg Asn Asp Met Cys His Ser Leu
 115 120 125
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 130 135 140
 Pro Pro Pro Thr Thr Thr Pro Glu Pro Thr Ala Pro Pro Arg Leu Gln
 145 150 155 160
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 165 170 175
 Tyr Ser Gly Ser Leu Gly Gly Thr Ile Ser Tyr Glu Ala Gln Asp Lys
 180 185 190
 Thr Gln Asp Leu Glu Asn Phe Leu Cys Asn Asn Leu Gln Cys Gly Ser
 195 200 205
 Phe Leu Lys His Leu Pro Glu Thr Glu Ala Gly Arg Ala Gln Asp Pro
 210 215 220
 Gly Glu Pro Arg Glu His Gln Pro Leu Pro Ile Gln Trp Lys Ile Gln
 225 230 235 240
 Asn Ser Ser Cys Thr Ser Leu Glu His Cys Phe Arg Lys Ile Lys Pro
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 Gln Lys Ser Gly Thr Arg Val Leu Ala Leu Leu Cys Ser Gly Phe Gln Pro
 260 265 270
 Lys Val Gln Ser Arg Leu Val Gly Gly Ser Ser Ile Cys Gln Gly Thr
 275 280 285
 Val Glu Val Arg Gln Gly Ala Gln Trp Ala Ala Leu Cys Asp Ser Ser
 290 295 300
 Ser Ala Arg Ser Ser Leu Arg Trp Glu Glu Val Cys Arg Glu Gln Gln
 305 310 315 320
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370 375 380
Leu Ala Leu Val Leu Leu Val Val Leu Leu Val Val Cys Gly Pro Leu
385 390 395 400
Ala Tyr Lys Lys Leu Val Lys Lys Phe Arg Gln Lys Lys Gln Arg Gln
405 410 415
Trp Ile Gly Pro Thr Gly Met Asn Gln Asn Met Ser Phe His Arg Asn
420 425 430
His Thr Ala Thr Val Arg Ser His Ala Glu Asn Pro Thr Ala Ser His
435 440 445 450
Val Asp Asn Glu Tyr Ser Gln Pro Pro Arg Asn Ser Arg Leu Ser Ala
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<212> PRT
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Lys Val Gln Asn Ile His Pro Val Glu Ser Ala Lys Ile Glu Pro Pro
35 40 45

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 85 90 95
 His His Val Arg Thr Lys Leu Asp Glu Leu Lys Arg Gln Glu Val Gly
 100 105 110
 Arg Leu Arg Met Leu Ile Lys Ala Leu Asp Ser Leu Gln Asp Ile
 115 120 125
 Gly Met Asp His Gln Ala Leu Leu Lys Gln Phe Asp His Leu Asn His
 130 135 140
 Leu Asn Pro Asp Lys Phe Glu Ser Thr Asp Leu Asp Met Leu Ile Lys
 145 150 155 160
 Ala Ala Thr Ser Asp Leu Glu His Tyr Asp Lys Thr Arg His Glu
 165 170 175
 Phe Lys Lys Tyr Glu Met Met Lys Glu His Glu Arg Arg Glu Tyr Leu
 180 185 190
 Lys Thr Leu Asn Glu Glu Lys Arg Lys Glu Glu Glu Ser Lys Phe Glu
 195 200 205
 Glu Met Lys Lys Lys His Glu Asn His Pro Lys Val Asn His Pro Gly
 210 215 220
 Ser Lys Asp Gln Leu Lys Glu Val Trp Glu Glu Thr Asp Gly Leu Asp
 225 230 235 240
 Pro Asn Asp Phe Asp Pro Lys Thr Phe Phe Lys Leu His Asp Val Asn
 245 250 255
 Ser Asp Gly Phe Leu Asp Glu Gln Glu Leu Glu Ala Leu Phe Thr Lys
 260 265 270
 Glu Leu Glu Lys Val Tyr Asp Pro Lys Asn Glu Glu Asp Met Val
 275 280 285
 Glu Met Glu Glu Glu Arg Leu Arg Met Arg Glu His Val Met Asn Glu
 290 295 300
 Val Asp Thr Asn Lys Asp Arg Leu Thr Leu Glu Glu Phe Lys Lys
 305 310 315 320
 Ala Thr Glu Lys Lys Glu Phe Leu Glu Pro Asp Ser Trp Glu Thr Leu
 325 330 335
 Asp Gln Gln Gln Phe Phe Thr Glu Glu Leu Lys Glu Tyr Glu Asn
 340 345 350
 Ile Ile Ala Leu Gln Gln Asn Glu Leu Lys Lys Ala Asp Glu Leu
 355 360 365
 Gln Lys Gln Lys Glu Glu Leu Gln Arg Gln His Asp Gln Leu Glu Ala
 370 375 380
 Gln Lys Leu Glu Tyr His Gln Val Ile Gln Gln Met Glu Gln Lys Lys
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35 40 45
Leu Val Lys Asp Cys Asp Gln His Arg Lys Ala Ala Cys Asp Pro
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Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His
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Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys
85 90 95
Thr Ile Thr Ala Asn Ala Glu Cys Ala Cys Arg Asn Gly Trp Gln Cys
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130 135 140
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145 150 155 160
Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr
165 170 175
His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile
180 185 190
Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala
195 200 205
Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser
210 215 220
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Ala Cys Ser Pro
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<212> DNA
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http://www.uspto.gov/patent

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 <213> Homo sapiens

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 Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
 35 40 45
 Arg Gly Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
 50 55 60
 Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
 65 70 75 80
 Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
 85 90 95
 Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
 100 105 110
 Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser
 115 120 125
 Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
 130 135 140
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 145 150 155 160
 Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
 165 170 175
 Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
 180 185 190
 Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro
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 Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
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35 40 45
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly
50 55 60
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln
65 70 75 80
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr
85 90 95
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val
100 105 110
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile
115 120 125
Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly
130 135 140
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser
145 150 155 160
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe
165 170 175
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys
180 185 190
Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu
195 200 205
Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
210 215 220

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<211> 2339
<212> DNA
<213> Homo sapiens

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<210> 103
<211> 567
<212> PRT
<213> Homo sapiens

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20 25 30
Val Pro Glu Gln Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
35 40 45
Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
50 55 60
Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
65 70 75 80
Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
85 90 95
Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
100 105 110
Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
115 120 125
Met Leu Gly His Leu Val His Leu Lys Asn Asp Cys His Phe Glu Glu
130 135 140
Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys Asp
145 150 155 160
Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys
165 170 175
Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His Glu
180 185 190
Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser
195 200 205
Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys
210 215 220
Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe
225 230 235 240
Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val
245 250 255
Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys
260 265 270
Val Ser Leu Leu Gln Asn Glu Val Glu Lys Asn Lys Ser Ile Gln
275 280 285
Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln
290 295 300
Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
305 310 315 320
Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
325 330 335 340
Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
345 350 355
Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
360 365
Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
370 375 380
Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp

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420 425 430
Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
435 440 445
Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
450 455 460
Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
465 470 475 480
Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
485 490 495
Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
500 505 510
Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
515 520 525
Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn
530 535 540
Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp
545 550 555 560
Thr Ser Asp Leu Pro Asp Pro
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<212> DNA
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<210> 105
<211> 155
<212> PRT
<213> Homo sapiens

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Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
35 40 45
Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
50 55 60
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
65 70 75
Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
85 90 95
Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
100 105 110
Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Glu Pro Pro His
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Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
130 135 140
Thr Cys Val Thr Pro Ile Val His His Val Ala
145 150 155

<210> 106
<211> 3120
<212> DNA
<213> Homo sapiens

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<210> 107
 <211> 866
 <212> PRT
 <213> Homo sapiens

<400> 107
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 Gly Leu Leu Leu Leu Leu Gly Val Leu Ala Pro Gly Gly Ala Ser
 20 25 30
 Leu Arg Leu Leu Asp His Arg Ala Leu Val Cys Ser Gln Pro Gly Leu
 35 40 45
 Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His
 50 55 60
 Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu
 65 70 75 80
 His Phe Ala His His Thr Gln Gln Gly Asp Leu Phe Pro Val Ala His Ile
 85 90 95
 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala
 100 105 110
 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg
 115 120 125
 Phe Glu Phe Leu Ser Lys Leu Arg His His His Arg Trp Arg Phe
 130 135 140
 Thr Phe Ser His Phe Val Val Asp Pro Asp Gln Tyr Gln Val Thr
 145 150 155
 Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln
 160 165 170
 Ser Lys Asn Phe Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val
 175 180 185
 Thr Thr Pro Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr
 190 195 200
 Val Glu Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp
 205 210 215
 Asn Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met
 220 225 230 235
 Glu Asn His Ser Cys Phe Glu His Met His His Ile Pro Ala Pro Arg
 240 245 250 255
 Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu Arg Asn
 260 265 270
 Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro Phe Phe Ser
 275 280 285
 Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr Val Ser Cys Pro
 290 295 300
 Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp Tyr Met Pro Leu Trp
 305 310 315 320
 Val Tyr Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val
 325 330 335
 Ile Leu Leu Ile Val Cys Met Thr Trp Arg Leu Ala Gly Pro Gly Ser
 340 345 350
 Gln Lys Tyr Ser Asp Asp Thr Lys Tyr Thr Asp Gly Leu Pro Ala Ala
 355 360 365
 Asp Leu Ile Pro Pro Pro Leu Lys Pro Arg Lys Val Trp Ile Ile Tyr
 370 375 380
 Ser Ala Asp His Pro Leu Tyr Val Asp Val Val Leu Lys Phe Ala Gln

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 385 390 395 400
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 405 410 415
 Glu Gln Ala Ile Ser Glu Ala Gly Val Met Thr Trp Val Gly Arg Gln
 420 425 430
 Lys Gln Glu Met Val Glu Ser Asn Ser Lys Ile Ile Val Leu Cys Ser
 435 440 445
 Arg Gly Thr Arg Ala Lys Trp Gln Ala Leu Leu Gly Arg Gly Ala Pro
 450 455 460
 Val Arg Leu Arg Cys Asp His Gly Lys Pro Val Gly Asp Leu Phe Thr
 465 470 475 480
 Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro Ala Cys Phe
 485 490 495
 Gly Thr Tyr Val Val Cys Tyr Phe Ser Glu Val Ser Cys Asp Gly Asp
 500 505 510
 Val Pro Asp Leu Phe Gly Ala Ala Pro Arg Tyr Pro Leu Met Asp Arg
 515 520 525
 Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met Phe Gln Pro
 530 535 540
 Gly Arg Met His Arg Val Gly Glu Leu Ser Gly Asp Asn Tyr Leu Arg
 545 550 555 560
 Ser Pro Gly Gly Arg Gln Leu Arg Ala Ala Leu Asp Arg Phe Arg Asp
 565 570 575
 Trp Gln Val Arg Cys Pro Asp Trp Phe Glu Cys Glu Asn Leu Tyr Ser
 580 585 590
 Ala Asp Asp Gln Asp Ala Pro Ser Leu Asp Glu Glu Val Phe Glu Glu
 595 600 605
 Pro Leu Leu Pro Pro Gly Thr Ile Val Lys Arg Ala Pro Leu Val
 610 615 620
 Arg Glu Pro Gly Ser Gln Ala Cys Leu Ala Ile Asp Pro Leu Val Gly
 625 630 635 640
 Glu Glu Gly Gly Ala Ala Val Ala Lys Leu Glu Pro His Leu Gln Pro
 645 650 655
 Arg Gly Gln Pro Ala Pro Gln Pro Leu His Thr Leu Val Leu Ala Ala
 660 665 670
 Glu Glu Gly Ala Leu Val Ala Ala Val Glu Pro Gly Pro Leu Ala Asp
 675 680 685
 Gly Ala Ala Val Arg Leu Ala Leu Ala Gly Glu Gly Glu Ala Cys Pro
 690 695 700
 Leu Leu Gly Ser Pro Gly Ala Gly Arg Asn Ser Val Leu Phe Leu Pro
 705 710 715 720
 Val Asp Pro Glu Asp Ser Pro Leu Gly Ser Thr Pro Met Ala Ser
 725 730 735
 Pro Asp Leu Leu Pro Glu Asp Val Arg Glu His Leu Glu Gly Leu Met
 740 745 750
 Leu Ser Leu Phe Glu Gln Ser Leu Ser Cys Gln Ala Gln Gly Gly Cys
 755 760 765
 Ser Arg Pro Ala Met Val Leu Thr Asp Pro His Thr Pro Tyr Glu Glu
 770 775 780
 Glu Gln Arg Gln Ser Val Gln Ser Asp Gln Gly Tyr Ile Ser Arg Ser
 785 790 795 800
 Ser Pro Gln Pro Pro Glu Gly Leu Thr Glu Met Glu Glu Glu Glu Glu
 805 810 815
 Glu Glu Gln Asp Pro Gly Lys Pro Ala Leu Pro Leu Ser Pro Glu Asp
 820 825 830
 Leu Glu Ser Leu Arg Ser Leu Gln Arg Gln Leu Leu Phe Arg Gln Leu
 835 840 845
 Gln Lys Asn Ser Gly Trp Asp Thr Met Gly Ser Glu Ser Glu Gly Pro
 850 855 860
 Ser Ala
 865

<210> 108
 <211> 578
 <212> DNA
 <213> Homo sapiens
 <400> 108

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 gccattcagg tcatagcctg cagtgctaca actgtcctaa cccaactgct gactgcaaaa 180
 cagccgctcaa ttgttctatc gattttgatg cgtgtctcat taccaaaagct ggggtacaag 240
 tgtataacaa gtgttggaag tttagcattt gcaatttcaa cgacgtcaca accgccttga 300
 gggaaaaatga gctaacgtac tactgtcgca agaaggacct gtgtaacttt aacgaacagc 360
 ttgaaaatgg ttgggacatcc ttatcagaga aaacagttct tctgctgggt acccatttct 420
 ttggcagcagc ctggagcctt catccctaag tcaaccacag gagagccttc cccaattctc 480
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 atggatcctg ttgggaaaga ataaaattag cttagacca 578

<210> 109
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 109
 Met Gly Ile Gln Gly Gly Ser Val Leu Phe Gly Leu Leu Leu Val Leu
 1 5 10 15
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 20 25 30
 Asn Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe
 35 40 45
 Asp Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys
 50 55 60
 Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg
 65 70 75
 Glu Asn Glu Leu Thr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe
 80 85 90 95
 Asn Glu Gln Leu Glu Asn Gly Gly Thr Ser Leu Ser Glu Lys Thr Val
 100 105 110
 Leu Leu Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro
 115 120 125

<210> 110
 <211> 1048
 <212> DNA
 <213> Homo sapiens

<400> 110
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 tggctccggc cagcaacgtg actctgaaca tctctgagag cctgcctgag aactacaac 180
 aactaacctg gttttatact ttgcagcaga agattgtaga atgggattcc agaaaaatcta 240
 agtacttata atccaatttt aaaggcaggg tcagacttga tcttcagagt ggcgcactgt 300
 acatcttcaa ggtccagaaa gaggacaaca gcacctacat catgagggtg ttgaaaaaga 360
 ctggggaatga gcaagaatgg aagatcaagc tgcaagtgtc tgacctgtga cccaagcctg 420
 tcatacaaat tgagaagata gaagacatgg atgacaactg ttatctgtaa ctgtctatgt 480
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 agctccagaa cagtgctgct gaaaccaccc ttatgccaca taattactcc aggtgtttata 600
 ctgtccaagt ctgcacattc gtgacgagca agaattggca cgtctgcctc agtccacctc 660
 gtaccttgcc cgggtccttt ggagtagaat ggattgcaag ttggctagtg gtcacgggtc 720
 ccacattctt tggcctgtta ctacctgag atgagctctt ttaactcaag ggaacttca 780
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 ggttatattt taatttata tccctttggt gttttgtagt acacagagat tatagagata 960
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 taaaaagata taattataaa aaaaaaaa 1048

<210> 111
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 111
 Met Trp Ser Arg Gly Trp Asp Ser Cys Leu Ala Leu Glu Leu Leu Leu
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 Leu Pro Leu Ser Leu Leu Val Thr Ser Ile Gln Gly His Leu Val His

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 20 25 30
 Met Thr Val Val Ser Gly Ser Asn Val Thr Leu Asn Ile Ser Glu Ser
 35 40 45
 Leu Pro Glu Asn Tyr Lys Gln Leu Thr Trp Phe Tyr Thr Phe Asp Gln
 50 55 60
 Lys Ile Val Glu Trp Asp Ser Arg Lys Ser Lys Tyr Phe Glu Ser Lys
 65 70 75 80
 Phe Lys Gly Arg Val Arg Leu Asp Pro Gln Ser Gly Ala Leu Tyr Ile
 85 90 95
 Ser Lys Val Gln Lys Glu Asp Asn Ser Thr Tyr Ile Met Arg Val Leu
 100 105 110
 Lys Lys Thr Gly Asn Glu Gln Glu Trp Lys Ile Lys Leu Gln Val Leu
 115 120 125
 Asp Pro Val Pro Lys Pro Val Ile Lys Ile Glu Lys Ile Glu Asp Met
 130 135 140
 Asp Asp Asn Cys Tyr Leu Lys Leu Ser Cys Val Ile Pro Gly Ser
 145 150 155 160
 Val Asn Tyr Thr Trp Tyr Gly Asp Lys Arg Pro Phe Pro Lys Glu Leu
 165 170 175
 Gln Asn Ser Val Leu Glu Thr Thr Leu Met Pro His Asn Tyr Ser Arg
 180 185 190
 Cys Tyr Thr Cys Gln Val Ser Asn Ser Val Ser Ser Lys Asn Gly Thr
 195 200 205
 Val Cys Leu Ser Pro Pro Cys Thr Leu Ala Arg Ser Phe Gly Val Glu
 210 215 220
 Trp Ile Ala Ser Trp Leu Val Val Thr Val Pro Thr Ile Leu Gly Leu
 225 230 235 240
 Leu Leu Thr

<210> 112
 <211> 1040
 <212> DNA
 <213> Homo sapiens

<400> 112
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 tgcctgtctgc actgctttgg ttcatcagc tgtttttccc aacaaatata tgggtgttgg 120
 taatgggaatg taactttcca tgtaccaagc aatgtgcctt taaaagaggt cctatggaaa 180
 aaaaataagg ataaagtgg agaactggaa aatctgaat tcagagcttt ctcactcttt 240
 tcagatgaag atgagtatga aatggaatcg ccaaatatta ctgataccat gaagttcttt 300
 cttttatgtgc ttgagctctt tccatctccc acactaaact gtgcattgac taatggaagc 420
 attgaagtcc aatgcattgat accagagcat tacacaagcc atcgaggact tataatgtac 480
 tcattgggatt gtcctatgga gcaatgtaaa cgtaactcaa ccagatatata ttttaagatg 540
 gaaaaatgat ttccacaaaa aatacagtggt actcttagca atccattatt taatacaaca 600
 tcatcaatca ttttgacaac ctgtatccca agcagcggtc attcaagaca cagatatgca 660
 ctatataccca taccattagc agtaattaca acatgtattg tgctgtatat gaatggtatt 720
 ctgaaatgtg acagaaaaacc agacagaaacc aactccaatt gatttgtaac agaagatgaa 780
 gacaacagca taactaaatt attttaaaaa ctaaaaagcc atctgatttc tcatgtgagt 840
 attacaattt tgaacaact gttggaaatg taacttgaag cagctgcttt aagaagaaat 900
 acccactaac aaagaacaag cattagtttt ggctgctatc aacttattat atgactaggt 960
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 tgtaaatagt tacacaagtg

<210> 113
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 113
 Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
 1 5 10 15
 Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
 20 25 30
 Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
 35 40 45
 Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
50          55          60
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
65 Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
          70          75          80
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
          85          90          95
Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
          100          105          110
Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
          115          120          125
Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
          130          135          140
145 Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
          145          150          155
Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
          160          165          170
Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
          175          180          185
Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
          190          195          200
Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
          205          210          215
225 Asp Arg Lys Pro Asp Thr Asn Ser Asn
          220          225          230
          235          240          245
          250
<210> 114
<211> 1358
<212> DNA
<213> Homo sapiens

<400> 114
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tgcgctttgtt gaaagtgcct ctgaagaaca gcgcattcaa ccatctagga caggactgtg 120
aggcctatga agatggggaa ctcacctacg agaactgca agtgtctcca gtcccaggag 180
ggccaccagg cttggcttcc cctgcactag cggacaaagc aggggtcggg tcagagcaac 240
caactgcgac ctggagctct gtgaagtcgt ctgctctcag gcagattccc cgctgtccta 300
cggctctgctt gcaaaacttc ttgcttggcc ttctctgtc ctgtctgatg ttagggtggtg 360
ctgtcatctg cctgggagtt cgctatctcg aggtgtctca gcagtccag gaggggacca 420
ggatttggga agccaccaat agcagctcgc agcagcagct cagggagaag ataagtccag 480
tggggcagaa ggaagtgga gctcaggagt ctcaagaaga gctgtatctc agccaggaca 540
cattacagga gaagcagagg actcacaagg acactgaga gcaactacaa gctgtccagg 600
ctgagagagc gaaagacca gagaacctga aacttgaga ggagcggagg agggacttgg 660
accagaggtt gacaagcacg cgggagacac tgaggcgctt ctctctctgt tcactcagca 720
cctgtctgtc atgcgagtag attccatatt aggaagggtg cttttacatc tcacataccc 780
tcagaagtct ggaggagagc caaaaatact gcacatctct gtctccaaa ctggcagcat 840
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ccagcggcctt agaggagtgt ctagatcggt cgaagtcata ttggatacag atgagcaaga 960
agtggaggca tgactatgac tctcaagcc gatattgtga caagataaaa aaattattacc 1020
agaagtggaa aagaacattt tctgagtgtg cagagcttca cccctgcatt tgtgagtcgg 1080
tgtgaacctac tctctcaact gggatccatc tgaactgaac cggatacttg aacacagact 1140
tgcctcactc atcccttaacc taaggctcgc caatttttaa gctgctattt cctccagcac 1200
cagaaactctg tggggcatcg ccagctaagg gatgaactgc tgcctgtctg aaagctgtct 1260
taaatacttc actactcttg ggaagagtta agaagctctc agaaaagact tgaccttctc 1320
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<210> 115
<211> 359
<212> PRT
<213> Homo sapiens

<400> 115
Met Ala Asp Ala Ile Thr Tyr Ala Asp Leu Arg Phe Val Lys Val Pro
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Leu Lys Asn Ser Ala Ser Asn His Leu Gly Gln Asp Cys Glu Ala Tyr
          20          25          30
Glu Asp Gly Glu Leu Thr Tyr Glu Asn Val Gln Val Ser Pro Val Pro
          35          40          45

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Gly Gly Pro Gly Leu Ala Ser Pro Ala Leu Ala Asp Lys Lys Ala Gly Val
50 55 60
Gly Ser Glu Gln Pro Thr Ala Thr Trp Ser Ser Val Lys Ser Ser Ala
65 70 75 80
Leu Arg Gln Ile Pro Arg Cys Pro Thr Val Cys Leu Gln Asn Phe Leu
85 90 95
Leu Gly Leu Leu Ser Cys Leu Met Leu Gly Val Ala Val Ile Cys
100 105 110
Leu Gly Val Arg Tyr Leu Gln Val Ser Gln Gln Phe Gln Gly Thr
115 120 125
Arg Ile Trp Glu Ala Thr Asn Ser Ser Leu Gln Gln Leu Arg Glu
130 135 140
Lys Ile Ser Gln Leu Gly Gln Lys Glu Val Glu Gln Glu Ser Gln Lys
145 150 155 160
Glu Leu Ile Ser Ser Gln Asp Thr Leu Gln Glu Lys Gln Arg Thr His
165 170 175
Lys Asp Thr Glu Gln Gln Leu Gln Ala Cys Gln Ala Glu Ala Lys
180 185 190
Thr Lys Glu Asn Leu Lys Thr Glu Glu Glu Arg Arg Asp Leu Asp
195 200 205
Gln Arg Leu Thr Ser Thr Arg Glu Thr Leu Arg Arg Leu Ser Ser Cys
210 215 220
Ser Ser Asp Thr Cys Cys Pro Cys Gly Trp Ile Pro Tyr Gln Glu Arg
225 230 235 240
Cys Phe Tyr Ile Ser His Thr Leu Arg Ser Leu Glu Glu Ser Gln Lys
245 250 255
Tyr Cys Thr Ser Leu Ser Ser Lys Leu Ala Ala Phe Asp Glu Pro Ser
260 265 270
Lys Tyr Tyr Glu Tyr Leu Ser Asp Ala Pro Gln Val Ser Leu Pro
275 280 285
Ser Gly Leu Glu Glu Leu Leu Asp Arg Ser Lys Ser Tyr Trp Ile Gln
290 295 300
Met Ser Lys Lys Trp Arg His Asp Tyr Asp Ser Gln Ser Arg Tyr Cys
305 310 315 320
Asp Lys Ile Lys Lys Tyr Tyr Gln Lys Trp Lys Arg Thr Phe Ser Glu
325 330 335
Cys Ala Glu Leu His Pro Cys Ile Cys Glu Ser Glu Ala Phe Arg Phe
340 345 350
Pro Asp Gly Ile His Leu Asn
355

<210> 116
<211> 856
<212> DNA
<213> Mus musculus

<400> 116
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ctgcatcgga catccccgag gtcttaaggg caggctcaagg cttcaaaagc 120
tcggctgagg aggctacacg ttcccgcctg cttcaggcgg ctgcttccgt gcagggatgc 180
cggaggaaagg tcgaccttgc ccttgggttc gctggagcgg gaccgcgttc cagcgccaat 240
ggcctatggct gctgctgggt gtgttttatta ctgtgttttg ctgttggttt catgtatgcg 300
gcactactcag taagcagcaa cagaggctgc tggagcaccc tgagccgcac acagctgagt 360
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ctttgggaag ctctctcaca caggaccagg agctggagga gggcattctg cgtatccatc 480
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gcaccttcga gcacagggcc accctggctg tgggcatctg ctcccgcgt gcgcacggca 600
tcagcttgct gcgtgggcgc ttgggacagg actgtacagt ggcattacag gccttgatc 660
accctgtcca cggagatgct ctctgtacca acctcaccct gcctctgtcg cgcgtccgca 720
acgctgatga caccctcttt ggagttcagt ggatgtgcc ttgaccacaa ctcaggatg 780
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taaaaaaaaa aaaaaa

<210> 117
<211> 195
<212> PRT
<213> Mus musculus

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<400> 117
Met Pro Glu Glu Gly Arg Pro Cys Pro Trp Val Arg Trp Ser Gly Thr
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Ala Phe Gln Arg Gln Trp Pro Trp Leu Leu Val Val Phe Ile Thr
20 25 30
Val Phe Cys Cys Trp Phe His Cys Ser Gly Leu Leu Ser Lys Gln Gln
35 40 45
Gln Arg Leu Leu Glu His Pro Glu Pro His Thr Ala Glu Leu Gln Leu
50 55 60
Asn Leu Thr Val Pro Arg Lys Asp Pro Thr Leu Arg Trp Gly Ala Gly
65 70 75 80
Pro Ala Leu Gly Arg Ser Phe Thr His Gly Pro Glu Leu Glu Gly
85 90 95
His Leu Arg Ile His Gln Asp Gly Leu Tyr Arg Leu His Ile Gln Val
100 105 110
Thr Leu Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu Gln His Arg Ala
115 120 125
Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ala His Gly Ile Ser Leu
130 135 140
Leu Arg Gly Arg Phe Gly Gln Asp Cys Thr Val Ala Leu Arg Leu
145 150 155 160
Thr Tyr Leu Val His Gly Asp Val Leu Cys Thr Asn Leu Thr Leu Pro
165 170 175
Leu Leu Pro Ser Asn Ala Asp Glu Thr Phe Phe Gly Val Gln Trp
180 185 190
Ile Cys Pro
195

<210> 118
<211> 909
<212> DNA
<213> Homo sapiens

<400> 118
atgcgctg gacgtctctg actgctcttc ctgctcttca gcagccttcg agctgatact 60
caggagaagg aagtcagagc gatggtaggc agcgacgtgg agctcagctg cgcttgcctc 120
gaaggaagcc gttttgatgtt aaatgatgtt tacgtatatt ggcaaacacc tgagtcgaaa 180
accgtggtga cctaccacat ccacacagaac agctccttgg aaaaagtggg cagccgctac 240
cggaaccgag ccctgatgtc accggccggc atgtctgggg gcgacttctc cctgcgcttg 300
ttcaaccgtca ccccccagga cgagcagaag ttctactgcc ttgtgtttgag ccaatccctg 360
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ataaacggct acccagggcc caactgtgtac tggatcaata agacggacaac cagctctgtg 540
gaccaggctc tgcagaatga caccgtcttc ttgaacatgc ggggcttcta tgacgtggtc 600
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aagatcacag agaattccagt cagtaccggc gagaaaaacg cgccacgtg gagcatcctg 780
gctgtcctgt gcctgctgtt ggtcgtggcg gtggccatag cctgggtgtg cagggaccga 840
tgctcccaac acagctatgc aggtgcctgg cgtgtgagtc cggagacaga gctcactggc 900
cacgtttga

<210> 119
<211> 302
<212> PRT
<213> Homo sapiens

<400> 119
Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15
Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30
Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45
Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60
Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80
Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Val Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

<210> 120
<211> 1424
<212> DNA
<213> Homo sapiens

<400> 120
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<210> 121
<211> 323
<212> PRT
<213> Homo sapiens

<400> 121
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Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	Leu	His	Asn	Leu	Gln	Ile
Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	His	His	Lys	Lys	Pro	Thr
Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser	Val	Leu	Ala
Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile	Thr	Glu	Asn
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Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	Ile	Glu	Tyr
Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	Tyr	Asp
Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	Ser	Asn	Met
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Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	Asp	His	Ile
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Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	Ser	Glu	Gln
Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	Asp	Glu	Ala
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Thr	Cys	Phe													

<210> 122
<211> 1816
<212> DNA
<213> Homo sapiens

<400> 122

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ccttctaaca ttaaaa 1816

<210> 123
<211> 261
<212> PRT
<213> Homo sapiens

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35 40 45
Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val
50 55 60
Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser
65 70 75 80
Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys
85 90 95
Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu
100 105 110
Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser
115 120 125
Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly
130 135 140
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln
145 150 155
Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr
160 165 170
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser
175 180 185 190
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala
195 200 205
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His
210 215 220
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn
225 230 235 240
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe
245 250 255
Gly Leu Leu Lys Leu
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<210> 124
<211> 1879
<212> DNA
<213> Homo sapiens

<400> 124
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<210> 125
<211> 400
<212> PRT
<213> Homo sapiens

<400> 125
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35 40 45
Ile Thr Ser Asp Pro Lys Ala Asp Ser Thr Gly Asp Gln Thr Ser Ala
50 55 60
Leu Pro Pro Ser Thr Ser Ile Asn Glu Gly Ser Pro Leu Trp Thr Ser
65 70 75
Ile Gly Ala Ser Thr Gly Ser Pro Leu Pro Glu Pro Thr Thr Tyr Gln
85 90 95
Glu Val Thr Ile Lys Met Ser Ser Val Pro Gln Glu Thr Pro His Ala
100 105 110
Thr Ser His Pro Ala Val Pro Ile Thr Ala Asn Ser Leu Gly Ser His
115 120 125
Thr Val Thr Gly Gly Thr Ile Thr Thr Asn Ser Pro Glu Thr Ser Ser
130 135 140
Arg Thr Ser Gly Ala Pro Val Thr Thr Ala Ala Ser Ser Leu Glu Thr
145 150 155
Ser Arg Gly Thr Ser Gly Pro Pro Leu Thr Met Ala Thr Val Ser Leu
160 165 170
Glu Thr Ser Lys Gly Thr Ser Gly Pro Pro Val Thr Met Ala Thr Asp
175 180 185
Ser Leu Glu Thr Ser Thr Gly Thr Thr Gly Pro Pro Val Thr Met Thr
190 195 200
Thr Gly Ser Leu Glu Pro Ser Ser Gly Ala Ser Gly Pro Gln Val Ser
205 210 215
Ser Val Lys Leu Ser Thr Met Met Ser Pro Thr Thr Ser Thr Asn Ala
220 225 230
Ser Thr Val Pro Phe Arg Asn Pro Asp Glu Asn Ser Arg Gly Met Leu
235 240 245
Pro Val Ala Val Leu Val Ala Leu Leu Ala Val Ile Val Leu Val Ala
250 255 260
Leu Leu Leu Leu Trp Arg Arg Arg Gln Lys Arg Arg Thr Gly Ala Leu
265 270 275
Val Leu Ser Arg Gly Gly Lys Arg Asn Gly Val Val Asp Ala Trp Ala
280 285 290
Gly Pro Ala Gln Val Pro Glu Glu Gly Ala Val Thr Val Thr Val Gly
295 300 305
Gly Ser Gly Gly Asp Lys Gly Ser Gly Phe Pro Asp Gly Glu Gly Ser
310 315 320
325 330 335

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Gln Gly Ser Leu Ala Met Glu Glu Leu Lys Ser Gly Ser Gly Pro Ser
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385 390 395 400

<210> 126
<211> 3567
<212> DNA
<213> Homo sapiens

<400> 126
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<210> 127
<211> 1038
<212> PRT
<213> Homo sapiens

<400> 127
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Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
35 40 45
Leu Tyr Glu Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
50 55 60
His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
65 70 75 80
Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
85 90 95
Cys Arg Ile Gly Lys Asn Pro Gly Glu Thr Cys Glu Glu Glu Leu
100 105 110
Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Arg
115 120 125
Asp Asn Glu Trp Leu Gly Val Thr Leu Ser Arg Glu Pro Gly Glu Asn
130 135 140
Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
145 150 155 160
Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
165 170 175
Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Glu Asp
180 185 190
Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Glu Ala Gly Ile
195 200 205
Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
210 215 220
Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
225 230 235 240
Tyr Lys Ala Phe Leu Asp Lys Glu Asn Glu Val Lys Phe Gly Ser Tyr
245 250 255
Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Glu His Thr Thr
260 265 270
Glu Val Val Gly Gly Ala Pro Glu His Glu Glu Ile Gly Lys Ala Tyr
275 280 285
Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys
290 295 300
Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp
305 310 315 320
Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Glu
325 330 335
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65 70 75
Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
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Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
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Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
115 120 125
Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
130 135 140
His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
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Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
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Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
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Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
205 210 215
Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
220 225 230
Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
235 240 245
Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu
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 35 40 45
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 50 55 60
 Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
 65 70 75
 Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
 80 85 90
 Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn
 95 100 105
 Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Gln Lys Trp
 110 115 120
 Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro His
 125 130 135
 Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr
 140 145 150
 Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp
 155 160 165
 Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser
 170 175 180
 Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro
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 200 205 210
 Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His
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 Thr Pro Lys Leu Gly Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg
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 245 250 255

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 Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser
 305 310 315
 Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val
 320 325 330
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 Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His
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 Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro
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 Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn
 385 390 395
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 400 405 410
 Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile
 415 420 425
 Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn
 430 435 440
 Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu
 445 450 455
 Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr
 460 465 470
 Thr Ile Ala Cys Ala Arg Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro
 475 480 485
 Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys
 490 495 500
 Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln
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 Cys Asp Phe Ser Ser Ser His Ser Lys Glu Val Gln Phe Thr Trp Glu
 520 525 530
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 535 540 545
 Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser Trp Val Asn Asn Ser
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 580 585 590
 Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val
 595 600 605
 Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro His His
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 625 630 635
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 685 690 695
 Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe Val Arg Asn Lys Lys
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<212> DNA
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<213> Homo sapiens

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35 40 45
Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg
50 55 60
Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly
65 70 75 80
Asn Cys Ser Glu Asp Leu Leu Cys Ile Leu Lys Arg Ala Pro Phe Lys
85 90 95
Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys
100 105 110
Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp
115 120 125
Gly Asn Leu Val Ile Gln Phe Pro Gly Leu Tyr Phe Ile Ile Cys Gln

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 165 170 175
 Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln
 180 185 190
 Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val
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 Leu Ser Ile Phe Leu Tyr Ser Asn Ser Asp
 225 230

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 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 50 55 60
 Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu
 65 70 75
 Lys Glu Leu Arg Cys Leu Leu Gly Leu Tyr Phe Gly Met Leu Leu Leu
 85 90 95
 Leu Phe Ala Thr Gln Ile Thr Leu Gly Ile Leu Ile Ser Thr Gln Arg
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 Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln
 115 120 125
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 130 135 140
 Tyr Val Gln Phe Gln Leu Arg Cys Cys Gly Trp His Tyr Pro Gln Asp
 145 150 155 160
 Trp Phe Gln Val Leu Ile Leu Arg Gly Asn Gly Ser Glu Ala His Arg
 165 170 175

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210 215 220
Ile Tyr Arg Glu Gly Cys Ala Gln Gly Leu Gln Lys Trp Leu His Asn
225 230 235 240
Asn Leu Ile Ser Ile Val Gly Ile Cys Leu Gly Val Gly Leu Leu Glu
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<210> 139
<211> 739
<212> PRT
<213> Homo sapiens

<400> 139
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 35 40 45
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 50 55 60
 Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Ser Thr Leu
 65 70 75 80
 Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr
 85 90 95
 Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile
 100 105 110
 Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu
 115 120 125
 Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro
 130 135 140
 Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys
 145 150 155 160
 Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys
 165 170 175
 Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val
 180 185 190
 Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro
 195 200 205
 Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Tyr Ile Ser Pro Lys
 210 215 220
 Asn Thr Val Ile Ser Val Asn Pro Ser Thr Lys Leu Gln Glu Gly Gly
 225 230 235 240
 Ser Val Thr Met Thr Cys Ser Ser Glu Gly Leu Pro Ala Pro Glu Ile
 245 250 255
 Phe Trp Ser Lys Lys Leu Asp Asn Gly Asn Leu Gln His Leu Ser Gly
 260 265 270
 Asn Ala Thr Leu Thr Leu Ile Ala Met Arg Met Glu Asp Ser Gly Ile
 275 280 285
 Tyr Val Cys Glu Gly Val Asn Glu Ile Gly Lys Asn Arg Lys Glu Val
 290 295 300
 Glu Leu Ile Val Gln Glu Lys Pro Phe Thr Val Glu Ile Ser Pro Gly
 305 310 315 320
 Pro Arg Ile Ala Ala Gln Ile Gly Asp Ser Val Met Leu Thr Cys Ser
 325 330 335
 Val Met Gly Cys Glu Ser Pro Ser Phe Ser Trp Arg Thr Gln Ile Asp
 340 345 350
 Ser Pro Leu Ser Gly Lys Val Arg Ser Glu Gly Thr Asn Ser Thr Leu
 355 360 365
 Thr Leu Ser Pro Val Ser Phe Glu Asn Glu His Ser Tyr Leu Cys Thr
 370 375 380
 Val Thr Cys Gly His Lys Lys Leu Glu Lys Gly Ile Gln Val Glu Leu
 385 390 395 400
 Tyr Ser Phe Pro Arg Asp Pro Glu Ile Glu Met Ser Gly Gly Leu Val
 405 410 415
 Asn Gly Ser Ser Val Thr Val Ser Cys Lys Val Pro Ser Val Tyr Pro
 420 425 430
 Leu Asp Arg Leu Glu Ile Glu Leu Leu Lys Gly Glu Thr Ile Leu Glu
 435 440 445
 Asn Ile Glu Phe Leu Glu Asp Thr Asp Met Lys Ser Leu Glu Asn Lys
 450 455 460
 Ser Leu Glu Met Thr Phe Ile Pro Thr Ile Glu Asp Thr Gly Lys Ala
 465 470 475 480
 Leu Val Cys Gln Ala Lys Leu His Ile Asp Asp Met Glu Phe Glu Pro
 485 490 495
 Lys Gln Arg Gln Ser Thr Gln Thr Leu Tyr Val Asn Val Ala Pro Arg
 500 505 510
 Asp Thr Thr Val Leu Val Ser Pro Ser Ser Ile Leu Glu Glu Gly Ser
 515 520 525
 Ser Val Asn Met Thr Cys Leu Ser Gln Gly Phe Pro Ala Pro Lys Ile
 530 535 540
 Leu Trp Ser Arg Gln Leu Pro Asn Gly Glu Leu Gln Pro Leu Ser Glu
 545 550 555 560
 Asn Ala Thr Leu Thr Leu Ile Ser Thr Lys Met Glu Asp Ser Gly Val

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 Glu Leu Ile Ile Gln Val Thr Pro Lys Asp Ile Lys Leu Thr Ala Phe
 580 585 590
 Pro Ser Glu Ser Val Lys Glu Gly Asp Thr Val Ile Ile Ser Cys Thr
 595 600 605
 Cys Gly Asn Val Pro Glu Thr Trp Ile Ile Leu Lys Lys Lys Ala Glu
 610 615 620 625
 Thr Gly Asp Thr Val Leu Lys Ser Ile Asp Gly Ala Tyr Thr Ile Arg
 630 635 640
 Lys Ala Gln Leu Lys Asp Ala Gly Val Tyr Glu Cys Glu Ser Lys Asn
 645 650 655
 Lys Val Gly Ser Gln Leu Arg Ser Leu Thr Leu Asp Val Gln Gly Arg
 660 665 670 675
 Glu Asn Asn Lys Asp Tyr Phe Ser Pro Glu Leu Leu Val Leu Tyr Phe
 680 685 690
 Ala Ser Ser Leu Ile Ile Pro Ala Ile Gly Met Ile Ile Tyr Phe Ala
 700 705 710 715 720
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 725 730 735
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<210> 140

<211> 2986

<212> DNA

<213> Homo sapiens

<400> 140

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 tctatttctt attttaccag ctattattgt atgtgtcttt atgtaggata aatgaacata 2220
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<210> 141
 <211> 532
 <212> PRT
 <213> Homo sapiens

<400> 141
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 20 25 30
 Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys
 35 40 45
 Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Gln Thr Pro Leu
 50 55 60
 Pro Lys Lys Glu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
 65 70 75 80
 Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
 85 90 95
 Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
 100 105 110
 Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
 115 120 125
 Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
 130 135 140
 Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
 145 150 155 160
 Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Val Leu Val Arg
 165 170 175
 Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
 180 185 190
 Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
 195 200 205
 Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Gln Leu Val Ser Pro
 210 215 220
 Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp
 225 230 235 240
 Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
 245 250 255
 Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
 260 265 270
 Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
 275 280 285
 Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
 290 295 300
 Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro
 305 310 315 320
 Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
 325 330 335
 Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
 340 345 350
 Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser
 355 360 365
 Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
 370 375 380
 Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
 385 390 395 400

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 420 425 430
 Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr
 435 440 445
 Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly
 450 455 460
 Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu
 465 470 475 480
 Ile Val Ile Ile Thr Val Val Ala Ala Val Ile Met Gly Thr Ala
 485 490 495
 Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
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 Ala Thr Pro Pro
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 <211> 591
 <212> DNA
 <213> Mus musculus

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 <211> 196
 <212> PRT
 <213> Mus musculus

<400> 143
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 35 40 45
 Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu
 50 55 60
 Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala
 65 70 75 80
 Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr
 85 90 95
 Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr
 100 105 110
 Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr
 115 120 125
 Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val
 130 135 140
 Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln
 145 150 155 160
 Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu
 165 170 175
 Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys
 180 185 190
 Thr Glu Thr
 195